

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 21, 2003, 18:39:49 ; Search time 27 Seconds  
(without alignments)  
1150.584 Million cell updates/sec

Title: US-09-913-955a-1

Perfect score: 3958  
Sequence: 1 MEATGSSVETGKANKRQTR.....AFNCPNSTNRGMDSRLW 749

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwIsProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3952	99.8	749	1	PEX_HUMAN
2	3837	96.9	749	1	PEX_MOUSE
3	1283.5	32.4	749	1	NEP_HUMAN
4	1270.5	32.1	749	1	NEP_RABIT
5	1263.5	31.9	749	1	NEP_RAT
6	1262.5	31.9	749	1	NEP_CANPO
7	1259.5	31.8	749	1	NEP_MOUSE
8	1257	31.8	770	1	ECCE1_HUMAN
9	1243.5	31.4	754	1	ECCE1_RAT
10	1241.5	31.4	754	1	ECCE1_BOVIN
11	1221	30.8	787	1	ECCE2_HUMAN
12	1184	29.9	787	1	ECCE2_BOVIN
13	992	25.1	775	1	ECCE1_MOUSE
14	977	24.7	775	1	ECCE1_RAT
15	969.5	24.5	775	1	ECCE1_HUMAN
16	949	24.0	769	1	YCYL_CAEEL
17	597.5	15.1	732	1	KEIL_HUMAN
18	586	14.8	647	1	PEPO_LACHE
19	495	12.5	626	1	PEPO_LACIA
20	494	12.5	626	1	PEPO_LACIC
21	365	9.2	564	1	YSC6_STRGC
22	135.5	3.4	2077	1	TEGU_HSV6U
23	135	3.4	853	1	NAT1_YEAST
24	126.5	3.2	2077	1	TEGU_HSV6G
25	126	3.2	1545	1	YMH2_YEAST
26	121	3.1	490	1	Y032_BOBNU
27	120	3.0	863	1	GYRA_CAMEL
28	117	3.0	408	1	Y53_METIA
29	116.5	2.9	700	1	R1RL_BACSU
30	116.5	2.9	1270	1	VGLN_CHICK
31	116.5	2.9	1616	1	VIT1_CAEEL
32	116.5	2.9	1790	1	VIT1_ANTGR
33	116	2.9	725	1	R1RL_MYCNU

34	116	2.9	3587	1	SRFL_BACSU	P27206 bacillus su
35	115	2.9	882	1	RA50_PYREU	P58301 pyrococcus
36	114.5	2.9	3061	1	POLG_PYTHU	002963 p genome po
37	114	2.9	762	1	MNLI_YEAST	P39106 saccharomyc
38	114	2.9	2059	1	TEGU_HSV7J	P52362 human herpe
39	113.5	2.9	986	1	EPHE-STAEF	P07768 oryctolagus
40	112.5	2.8	1826	1	SUTS_RABIT	045894 clostridium
41	112	2.8	1295	1	BX42_CIOBO	P1928 splinacia ol
42	111.5	2.8	1056	1	SPS_SPIOT	P47037 saccharomyc
43	111.5	2.8	1230	1	SMC3_YEAST	P40383 schizosacch
44	111	2.8	1328	1	EXO2_SCHPO	P25439 drosophila
45	110	2.8	1638	1	BRM_DROME	

## ALIGNMENTS

RESULT 1  
ID PEX\_HUMAN STANDARD: PRT; 749 AA.  
AC P78562; C00678; Q99827; Q13646; Q93032;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update) (EC 3.4.24.-)  
DE Phosphate regulating neutral endopeptidase (PRN)  
DE (Metalloendopeptidase homolog PEX) (X-linked hypophosphatemia protein).  
DE (HYP) (Vitamin D-resistant hypophosphatemic rickets protein).  
GN PHEX OR PEX.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=97343325; PubMed=9199930;  
RP PRO-651  
RX FRANCIS F., Strom T.M., Hennig S., Boeddrich A., Lorenz B.,  
RA Brandau O., Mohlke K.L., Cagnoli M., Steffens C., Klages S.,  
RA Borzym K., Pohl T., Oudet C.L., Econs M.D., Rowe P.S.N., Reinhardt R.,  
RA Mellinger T., Lehrach H.;  
RT "Genomic organization of the human PEX gene mutated in X-linked  
RT dominant hypophosphatemic rickets";  
RL Genome Res. 7:573-585(1997).  
RN [2]  
RP MEDLINE=97323252; PubMed=9077527;  
RX Beck L., Soumounou Y., Martel J., Krishnamurthy G., Gauthier C.,  
RA Goodyer C.G., Tenenhouse H.S.;  
RT "PEX/PEX tissue distribution and evidence for a deletion in the 3'  
RT region of the Pex gene in X-linked hypophosphatemic mice";  
RL J. Clin. Invest. 99:1200-1209(1997).  
RN [3]  
RP MEDLINE=97343443; PubMed=9199999;  
RX TISSUE=bone;  
RA MEDLINE=97343443; PubMed=9199999;  
RT "Cloning and sequencing of human PEX from a bone cDNA library:  
RT evidence for its developmental stage-specific regulation in  
RT osteoblasts";  
RL J. Bone Miner. Res. 12:1009-1017(1997).  
RN [4]  
RP MEDLINE=97224400; PubMed=9070861;  
RX Grief M., Mumm S., Waeitz P., Mazzarella R., Whyte M.P.,  
RA Thakker R.V., Schlesinger D.;  
RT "Expression and cloning of the human X-linked hypophosphatemia gene  
RT cDNA";  
RL Biochem. Biophys. Res. Commun. 231:635-639(1997).

[6]  
 RP SEQUENCE OF 4-641 FROM N.A.  
 RX MEDLINE-96024647; PubMed-7550339;  
 RA Francis F., Hennig S., Korn B., Reinhardt R., de Jong P., Poustka A.,  
 RA Leirach H., Rowe P.S.N., Goulding J.N., Summerfield T., Mountford R.,  
 RA Econs M.J., Popowska E., Pronicka E., Davies K.E., Orlordan J.L.H.,  
 RA Hanaauer A., Strom T.M., Melndi A., Lorenz B., Cagnoli M.,  
 RA Mounine K.L., Murken J., Mellingner T.;  
 RT "A gene (PEX) with homologues to endopeptidases is mutated in  
 RT patients with X-linked hypophosphatemic rickets. The HYP  
 RT Consortium";  
 RL Nat. Genet. 11:130-136(1995).  
 RP [7]  
 RP SEQUENCE OF 1-116 FROM N.A.  
 RA Webster R.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RP [8]  
 RP VARIANTS HYP TYR-85; CYS-166; SER-252; ILE-253 AND VAL-579.  
 RX MEDLINE-97260404; PubMed-9106524;  
 RA Holm I.A., Huang X., Kunkel L.M.;  
 RT "Mutational analysis of the PEX gene in patients with X-linked  
 RT hypophosphatemic rickets";  
 RL Am. J. Hum. Genet. 60:790-797(1997).  
 RP [9]  
 RP VARIANTS HYP SER-77; PRO-138; LEU-534 AND ARG-579.  
 RX MEDLINE-97252387; PubMed-9097956;  
 RA Rowe P.S.N., Oudet C.L., Francis F., Stinding C., Pannetier S.,  
 RA Econs M.J., Strom T.M., Mellingner T., Garabedian M., David A.,  
 RA Macher M.A., Questiaux E., Popowska E., Pronicka E., Read A.P.,  
 RA Mokrzycki A., Glorieux F.H., Dreznier M.K., Hanaauer A., Lehnach H.,  
 RA Goulding J.N., O'Riordan J.L.H.;  
 RT "Distribution of mutations in the PEX gene in families with X-linked  
 RT hypophosphatemic rickets (HYP)";  
 RL Hum. Mol. Genet. 6:539-549(1997).  
 RP [10]  
 RP VARIANT HYP PRO-555.  
 RX MEDLINE-98439582; PubMed-9768646;  
 RA Econs M.J., Friedman N.E., Rowe P.S.N., Speer M.C., Francis F.,  
 RA Strom T.M., Oudet C.L., Smith J.A., Nimomiya J.T., Lee B.E.,  
 RA Bergen H.;  
 RT "A PHEX gene mutation is responsible for adult-onset vitamin  
 RT D-resistant hypophosphatemic osteomalacia: evidence that the disorder  
 RT is not a distinct entity from X-linked hypophosphatemic rickets";  
 RL J. Clin. Endocrinol. Metab. 83:3459-3462(1996).  
 RP [11]  
 RP VARIANTS HYP F-317; L-534; R-579; R-621; N-680 DEL; T-720; Y-731 AND  
 RP R-749.  
 RX MEDLINE-98439610; PubMed-9768674;  
 RA Dixon P.H., Christie P.T., Wooding C., Trump D., Gieff M., Holm I.A.,  
 RA Gertner J.M., Schmidtke J., Shan B., Shaw N., Smith C., Tau C.,  
 RA Schlesinger D., Whyte M.P., Thakker R.V.;  
 RT "Mutational analysis of PHEX gene in X-linked hypophosphatemia";  
 RL J. Clin. Endocrinol. Metab. 83:3615-3623(1998).  
 RP [12]  
 RP VARIANTS HYP S-80; F-142; G-237; C-530; D-573; S-733 AND W-746.  
 RX MEDLINE-99368844; PubMed-10439971;  
 RA Filisetti D., Ostermann G., von Bredow M., Strom T.M., Filler G.,  
 RA Ehrlich J., Pannetier S., Garnier J.-M., Rowe P.S.N., Francis F.,  
 RA Jullienne A., Hanaauer A., Econs M.J., Oudet C.L.,  
 RT "Non-random distribution of mutations in the PHEX gene, and  
 RT under-detected missense mutations at non-conserved residues";  
 RL Eur. J. Hum. Genet. 7:615-619(1999).  
 RP [13]  
 RP VARIANTS HYP F-85; P-141; V-341 DEL; P-567; K-680 AND Y-693.  
 RX MEDLINE-20202840; PubMed-10737991;  
 RA Tyymismaa H., Kattila I., Naentoe-Salonen K., Ala-Houhaja M.,  
 RA Alitalo T.;  
 RT "Identification of fifteen novel PHEX gene mutations in Finnish  
 RT patients with hypophosphatemic rickets";  
 RL Hum. Mutat. 15:383-384(2000).  
 RP [14]  
 RP VARIANTS HYP ARG-160 AND ASN-444 INS.

RX MEDLINE-20461419; PubMed-11004247;  
 RA Sato K., Tajima T., Nakae J., Adachi M., Asakura Y., Tachibana K.,  
 RA Suwa S., Katsumata N., Tanaka T., Hayashi Y., Abe S., Muraishi M.,  
 RA Okhara K., Shinohara N., Fujieda K.;  
 RT "Three novel PHEX gene mutations in Japanese patients with X-linked  
 RT hypophosphatemic rickets";  
 RL Pediatr. Res. 48:536-540(2000).  
 RP [15]  
 RP FUNCTION: PROBABLY INVOLVED IN BONE AND DENTIN MINERALIZATION  
 RP AND RENAL PHOSPHATE REABSORPTION.  
 RP SUBCELLULAR LOCATION: Type II membrane protein (potential).  
 RP TISSUE SPECIFICITY: LYMPHOCYTE AND FETAL BRAIN; NOT IN ADULT  
 RP BRAIN, PLACENTA, SKELETAL MUSCLE, AND PANCREAS; NOT IN ADULT AND  
 RP FETAL HEART, LUNG, LIVER, AND KIDNEY.  
 RP DISEASE: DEFECTS IN PHEX ARE A CAUSE OF X-LINKED HYPOPHOSPHATEMIC  
 RP RICKETS (HYP), A DOMINANT DISORDER CHARACTERIZED BY IMPAIRED  
 RP PHOSPHATE UPTAKE IN THE KIDNEY, WHICH IS LIKELY TO BE CAUSED BY  
 RP ABNORMAL REGULATION OF SODIUM PHOSPHATE COTRANSPORT IN THE  
 RP PROXIMAL TUBULES. CLINICAL MANIFESTATIONS INCLUDE SKELETAL  
 RP DEFORMITIES, GROWTH FAILURE, CRANIOSTOSIS, PARAVERTEBRAL  
 RP CALCIFICATIONS, PSEUDOFRACTURES IN LOWER EXTREMITIES, AND MUSCULAR  
 RP HYPOTONIA WITH ONSET IN EARLY CHILDHOOD. X-LINKED HYPOPHOSPHATEMIC  
 RP RICKETS IS THE MOST COMMON FORM OF HYPOPHOSPHATEMIA WITH AN  
 RP INCIDENCE OF 1 IN 20000.  
 RP [16]  
 RP SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.  
 RP [17]  
 RP DATABASE: NAME-PHEXdb; WWW="http://data.mcgill.ca/phexdb/".  
 RP [18]  
 RP This SWISS-PROT entry is copyright. It is produced through a collaboration  
 RP between the Swiss Institute of Bioinformatics and the EMBL outstation  
 RP the European Bioinformatics Institute. There are no restrictions on its  
 RP use by non-profit institutions as long as its content is in no way  
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 RP or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL: Y10196; CA671258.1; -  
 DR EMBL: U75645; AAB47749.1; -  
 DR EMBL: U82970; AAC24487.1; -  
 DR EMBL: U87284; AAB47562.1; -  
 DR EMBL: Y08111; CA669326.1; -  
 DR EMBL: Y08112; CA669326.1; JOINED.  
 DR EMBL: Y08113; CA669326.1; JOINED.  
 DR EMBL: Y08114; CA669326.1; JOINED.  
 DR EMBL: Y08115; CA669326.1; JOINED.  
 DR EMBL: Y08116; CA669326.1; JOINED.  
 DR EMBL: Y08117; CA669326.1; JOINED.  
 DR EMBL: Y08118; CA669326.1; JOINED.  
 DR EMBL: Y08119; CA669326.1; JOINED.  
 DR EMBL: Y08120; CA669326.1; JOINED.  
 DR EMBL: Y08121; CA669326.1; JOINED.  
 DR EMBL: Y08122; CA669326.1; JOINED.  
 DR EMBL: Y08123; CA669326.1; JOINED.  
 DR EMBL: Y08124; CA669326.1; JOINED.  
 DR EMBL: Y08125; CA669326.1; JOINED.  
 DR EMBL: Y08126; CA669326.1; JOINED.  
 DR EMBL: Y08127; CA669326.1; JOINED.  
 DR EMBL: Y08128; CA669326.1; JOINED.  
 DR EMBL: Y08129; CA669326.1; JOINED.  
 DR EMBL: Y08130; CA669326.1; JOINED.  
 DR EMBL: Y08131; CA669326.1; JOINED.  
 DR EMBL: Y08132; CA669326.1; JOINED.  
 DR EMBL: Y08133; AAB42219.1; JOINED.  
 DR EMBL: Y08134; AAB42219.1; JOINED.  
 DR EMBL: Y08135; AAB42219.1; JOINED.  
 DR EMBL: Y08136; AAB42219.1; JOINED.  
 DR EMBL: Y08137; AAB42219.1; JOINED.  
 DR EMBL: Y08138; AAB42219.1; JOINED.  
 DR EMBL: Y08139; AAB42219.1; JOINED.  
 DR EMBL: Y08140; AAB42219.1; JOINED.  
 DR EMBL: Y08141; AAB42219.1; JOINED.  
 DR EMBL: Y08142; AAB42219.1; JOINED.  
 DR EMBL: Y08143; AAB42219.1; JOINED.  
 DR EMBL: Y08144; AAB42219.1; JOINED.  
 DR EMBL: Y08145; AAB42219.1; JOINED.  
 DR EMBL: Y08146; AAB42219.1; JOINED.  
 DR EMBL: Y08147; AAB42219.1; JOINED.  
 DR EMBL: Y08148; AAB42219.1; JOINED.  
 DR EMBL: Y08149; AAB42219.1; JOINED.  
 DR EMBL: Y08150; AAB42219.1; JOINED.



FT CARBOHYD 736 736 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CONFLICT 430 430 D -> V (IN REF. 3).  
 SQ SEQUENCE 749 AA; 86418 MM; A88FA481C376C18A CRC64;  
 Query Match  
 Best Local Similarity 96.9%; Score 3837; DB 1; Length 749;  
 Matches 718; Conservative 20; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MEATGSSVETKKGKNGRTIAVAVGCTIYGLTILFLVSGGLSLQAKOBYCCKPCCI 60  
 DB 1 MEATGSSVETKKGKNGRTIAVAVGCTIYGLTILFLVSGGLSLQAKOBYCCKPCCI 60  
 QY 61 EAAALISKVNLSDPCDNFFRACDGMISNNPIEDMPSYGVYWLHNNDIKELLE 120  
 DB 61 EAAALISKVNLSDPCDNFFRACDGMISNNPIEDMPSYGVYWLHNNDIKELLE 120  
 QY 121 KSISRRTDEALQAKITLSSCMNEKALEKADAKPLHLRHSRPMPLVSNIGPEGW 180  
 DB 121 KSISRRTDEALQAKITLSSCMNEKALEKADAKPLHLRHSRPMPLVSNIGPEGW 180  
 QY 121 KSISRRTDEALQAKITLSSCMNEKALEKADAKPLHLRHSRPMPLVSNIGPEGW 180  
 DB 121 KSISRRTDEALQAKITLSSCMNEKALEKADAKPLHLRHSRPMPLVSNIGPEGW 180  
 QY 181 SERKESLQTLATFRGOYSNSVFIRLYVSPDKASNEHILKDLQATSLANREDYDNT 240  
 DB 181 SERKESLQTLATFRGOYSNSVFIRLYVSPDKASNEHILKDLQATSLANREDYDNT 240  
 QY 241 EAKSYRDALYKFMVDTAVLLGANSRAHDKSVLRLEIKIAETIMPHENTSEAMYK 300  
 DB 241 EAKSYRDALYKFMVDTAVLLGANSRAHDKSVLRLEIKIAETIMPHENTSEAMYK 300  
 QY 301 NISELSAMIPQDWLGYIKYIDRLYPLKDISPENYVRYQYKDFLLGSRKK 360  
 DB 301 NISELSAMIPQDWLGYIKYIDRLYPLKDISPENYVRYQYKDFLLGSRKK 360  
 QY 361 TIANTLVRYMYSRIPNLSRREORYRLEFSVIGTITLLPQWDKCVNFESALPYVVK 420  
 DB 361 TIANTLVRYMYSRIPNLSRREORYRLEFSVIGTITLLPQWDKCVNFESALPYVVK 420  
 QY 421 MEUVYVQEOCKEMEEELVSGVNAFTDMEKENEMMDAGTKRKAERKAVIATKYGE 480  
 DB 421 MEUVYVQEOCKEMEEELVSGVNAFTDMEKENEMMDAGTKRKAERKAVIATKYGE 480  
 QY 481 FIMNDTVNEDIAIKFSEADYFGNYLQTKYLAOSDFWLRKAVKTEMTNPTVNAF 540  
 DB 481 FIMNDTVNEDIAIKFSEADYFGNYLQTKYLAOSDFWLRKAVKTEMTNPTVNAF 540  
 QY 541 YSASTNIRPAGELQKPFMGTEPRSLSYGAIYVGHETFGDNNGRYDNGMD 600  
 DB 541 YSASTNIRPAGELQKPFMGTEPRSLSYGAIYVGHETFGDNNGRYDNGMD 600  
 QY 601 PMSSESEKFEKTKCMINOSNYWKAGLVNAGKRTIGENIADNGCLREAFRAVYK 660  
 DB 601 PMSSESEKFEKTKCMINOSNYWKAGLVNAGKRTIGENIADNGCLREAFRAVYK 660  
 QY 661 INDRGGLLEPLPGITFTNNOLFELSAHVACNSYREPEAREVOYGAHSPPFRVNGA 720  
 DB 661 INDRGGLLEPLPGITFTNNOLFELSAHVACNSYREPEAREVOYGAHSPPFRVNGA 720  
 QY 721 ISNSEFOAFNCPNPNSTNNRGMSCRLM 749  
 DB 721 ISNSEFOAFNCPNPNSTNNRGMSCRLM 749  
 RESULT 3  
 NEP\_HUMAN  
 ID NEP\_HUMAN STANDARD; PRT; 749 AA.  
 AC P08473;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neprilysin (EC 3.4.24.11) (Neutral endopeptidase)  
 DE (Enkephalinase) (Common acute lymphocytic leukemia antigen) (CALLA)  
 DE (Neutral endopeptidase 24.11) (CD10).  
 GN MME OR EFN.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 2-749 FROM N.A.  
 RC TISSUE-Placenta;  
 RX MEDLINE=88152222; PubMed=3162217;  
 RA Malfroy B., Kuang W.-J., Seeburg P.H., Mason A.J., Schofield P.R.,  
 RT "Molecular cloning and amino acid sequence of human enkephalinase  
 (neutral endopeptidase).";  
 RL FEBS Lett. 229:206-210(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Kidney;  
 RX MEDLINE=89010526; PubMed=2971756;  
 RA Letarte M., Vera S., Tran R., Addis J.B.L., Onizuka R.J.,  
 RT Quackenbush E.J., Jongeneel C.V., McInnes R.R.;  
 RL "Common acute lymphocytic leukemia antigen is identical to neutral  
 endopeptidase.";  
 RN [3]  
 RP J. Exp. Med. 166:1247-1253(1988).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88263038; PubMed=2968607;  
 RA Shipp M.A., Richardson N.E., Sayre P.H., Brown N.R., Masteller E.L.,  
 RT Clayton L.K., Ritz J., Reinherz E.L.;  
 RL "Molecular cloning of the common acute lymphoblastic leukemia antigen  
 (CALLA) identifies a type II integral membrane protein.";  
 RN [5]  
 RP Proc. Natl. Acad. Sci. U.S.A. 85:4819-4823(1988).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8938688; PubMed=2528730;  
 RA D'Amato L., Shipp M.A., Masteller E.L., Reinherz E.L.;  
 RT "Organization of the gene encoding common acute lymphoblastic  
 leukemia antigen (neutral endopeptidase 24.11): multiple minixons  
 and separate 5' untranslated regions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7103-7107(1989).  
 RN [7]  
 RP ACTIVE SITE ASP-650.  
 RX MEDLINE=94222095; PubMed=8168535;  
 RA Le Monal H., Dion N., Roques B.P., Crine P., Boileau G.;  
 RT "Asp650 is crucial for catalytic activity of neutral endopeptidase  
 24-11.";  
 RL Eur. J. Biochem. 221:475-480(1994).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RX MEDLINE=20135972; PubMed=1068592;  
 RA Oefner C., D'Arcy A., Hennig M., Winkler F.K., Dale G.E.;  
 RT "Structure of human neutral endopeptidase (Neprilysin) complexed with  
 phosphoramidon.";  
 RL J. Mol. Biol. 296:341-349(2000).  
 CC -1- FUNCTION: THERMOLYSIN-LIKE SPECIFICITY, BUT IS ALMOST CONFINED ON  
 ACTING ON POLYPEPTIDES OF UP TO 30 AMINO ACIDS. BIOLOGICALLY  
 IMPORTANT IN THE DESTRUCTION OF OPIOID PEPTIDES SUCH AS MET-  
 AND LEU-ENKEPHALINS BY CLEAVAGE OF A GLY-PHE BOND.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage at the amino group of  
 hydrophobic residues in insulin, casein, hemoglobin, and a number  
 of other proteins and polypeptides.  
 CC -1- COFACTOR: BINDS 1 ZINC ION.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- DISEASE: IMPORTANT CELL SURFACE MARKER IN THE DIAGNOSTIC OF HUMAN  
 ACUTE LYMPHOBLASTIC LEUKEMIA.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.  
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 DR EMBL: X07166; CAA30157.1; ALT\_INIT.  
 DR EMBL: Y00811; CAA68752.1; -.



OY		131	AIOCAKLLYSGCCNKEKAIEKADAPLHLILRSPPRWLYLESNTGPGVMSER-----KEST	187
Db		131	AVOQAKMLYNSCINESAIDSERGEPELTKL-LPDIYGMPATEN-----WEOKIGASWTA	193
OY		188	LQTLATRGQSYNSFYRLRYSPDDCAASHHILIKIDQATLSIAVEDYLDNSTEAKSYRD	247
Db		184	EKAIAOLNSKTKGVVLINLFVGTDCKSNVNYHIHDQPLGPSR-DYEECTGLYREACT	242
OY		248	ALYKEMVDTVL-----LGANSSRAEHDKSVYLRIETKIAELMIPHNRTSE-AMYNKM	300
Db		243	AYVPMISVALLIHQEERLPIDEKQLALENNKVMLEKETIANTAKPEDRNDPLLITIKYM	302
OY		301	NISELSAMI-----PODWIGYIKKYIDRLPYLHKDISPSENVYVRVQYKDFRIL	354
Db		303	TLAQIONNSELEINGKRPFWLNFTNEIMSYNI-----SITNEDEVVYAPELVITKIPIL	358
OY		355	GSEKKTIANYLVWRMYVSRIPIUSRRQYRMLEFSKVIOGTTLTLPDMDCVNFIESAL	414
Db		359	TKYSADNLONLMSPFINDIVSLSRTRYKESRNMFRAALGTTSETAIRRCANINYGNM	418
OY		415	PYYVGKAFDYVFQDDKKNMEDELVEGRNAFIOMLEKENEMDAGTKRKAKARAVYA	474
Db		419	ENAVGHLYEAFAAGESKAYVEDLIAQIREVFIGTLD-DLTMWDAEFKKAEKALAIKE	477
OY		475	KVGP-EFYMDTHVNEDLKAIKFESEADYEGNVIQTRKIYLAOSPFWLRAVYKTSMFPN	533
Db		478	RIGPDIDYNSDKLIKNEYLEANEYDEDEFENIIONKFOSOKOLKLRKVKNDKEMIG	537
OY		534	PTYNAFYASTNQIIFEPAGELOKPFEMOTEXPRLSGAIGVTIGHETHFGDNGNRKI	593
Db		538	AAVANAFTSGRGNOYTFPAGIIAPPFF-SAOOSNLANLGGICMGVIHEITHGFDDNGRNF	596
OY		594	DKNCNLDPWWSTSESEKFEKTKCOMINOYSNYWKKA-GLVKKRGTIGENTIANGLARE	652
Db		597	NKDODDIVDMWTQOASAFSESOCMVYOYOGNSWDLAGGOHLNGINTLIGEIMIANGLGQ	656
OY		653	APRAYKWINDROGLPEPLPIGITFTNNQOLFELSYAHVCNSYRPEARBOVOIGASP	712
Db		657	AYRAYONI--KKKG-BEKILLPGIDLNHKQFLFNACQWCSTGYPEYVAVNSIKTDVHP	713
OY		713	POFRVNGAISNSEEFQAKFNCPPNSTWNRCMDSCLW	749
Db		714	GNFRITIGLONSASFESAFHCNKSYMN-BEKKCRWV	749
<hr/>				
RESULT 4				
NEP_RABBIT				
ID	NEP_RABBIT	STANDARD;	PRT;	749 AA.
AC	P08049:			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)			
DE	(Enkephalinase) (Neutral endopeptidase 24.11).			
GN	MME.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=Kidney;			
RX	MEDLINE=87215825; PubMed=2440677;			
RA	Devaull A., Lazure C., Nault C., Le Moual H., Seidah N.G.,			
RA	Chretien M., Kahn P., Powell J., Mallet J., Beaumont A., Roques B.P.,			
RA	Crine P., Boileau G.;			
RT	"amino acid sequence of rabbit kidney neutral endopeptidase 24.11			
RT	(enkephalinase) deduced from a complementary DNA."			
RL	EMBO J. 6:1317-1322(1987).			
RN	[2]			
RP	ERRATUM.			
RA	Devaull A., Lazure C., Nault C., Le Moual H., Seidah N.G.,			
RA	Chretien M., Kahn P., Powell J., Mallet J., Beaumont A., Roques B.P.,			

RA Crine P., Bolleau G.;  
 RL EMBL J. 6:2506-2506(1987).  
 RN [3]  
 RP SEQUENCE OF 205-273 FROM N.A.  
 RX MEDLINE-87241344; PubMed-3297057;  
 RA Kahn P.H., Powell J.F., Beaumont A., Roques B.P., Mallet J.J.;  
 RT "An antibody purified with a lambda CII fusion protein precipitates  
 RL encephalinase activity";  
 RN Biochem. Biophys. Res. Commun. 145:488-493(1987).  
 RP NOTAGNESIS  
 RX MEDLINE-88196403; PubMed-3162886;  
 RA Devault A., Sales V., Nault C., Beaumont A., Roques B., Crine P.,  
 RA Bolleau G.;  
 RT Exploration of the catalytic site of endopeptidase 24.11 by site-  
 RT directed mutagenesis. Histidine residues 583 and 587 are essential  
 RL for catalysis";  
 RN FEBS Lett. 231:54-58(1988).  
 CC -1- FUNCTION: THERMOLYSIN-LIKE SPECIFICITY, BUT IS ALMOST CONFINED ON  
 CC ACTING ON POLYPEPTIDES OF UP TO 30 AMINO ACIDS. BIOLOGICALLY  
 CC IMPORTANT IN THE DESTRUCTION OF OPIOID PEPTIDES SUCH AS MET-  
 CC AND LEO-ENKEPHALINS BY CLEAVAGE OF A GLY-PHE BOND.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage at the amino group of  
 CC hydrophobic residues in insulin, casein, hemoglobin, and a number  
 CC of other proteins and polypeptides.  
 CC -1- COFACTOR: BINDS 1 ZINC ION.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL: X05338; CAA28950.1; -  
 DR EMBL: M18593; AAA53694.1; -  
 DR PIR: A29451; HYBN.  
 DR HSSP: P08473; 1DMT.  
 DR MEROPS: M13.001; -  
 DR InterPro: IPR000718; Peptidase\_M13.  
 DR InterPro: IPR001230; Ptenyl\_site.  
 DR InterPro: IPR000130; Zn\_Metpeptase.  
 DR Pfam: PF01431; Peptidase\_M13; 1.  
 DR PRINTS: PR00786; NEPRILYSIN.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 KW Hydrolyase; Metalloprotease; zinc; Transmembrane; Glycoprotein;  
 KW Signal-anchor.  
 FT INIT\_MET 0  
 FT DOMAIN 1 27  
 FT TRANSMEM 28 50  
 FT DOMAIN 51 749  
 FT DOMAIN 15 22  
 FT BINDING 102 102  
 FT METAL 583 583  
 FT ACT\_SITE 584 584  
 FT METAL 587 587  
 FT METAL 646 646  
 FT ACT\_SITE 650 650  
 FT CARBOHYD 144 144  
 FT CARBOHYD 284 284  
 FT CARBOHYD 310 310  
 FT CARBOHYD 324 324  
 FT CARBOHYD 627 627  
 FT SEQUENCE 749 AA; 85450 MW; E60B04357B0BAB96 CMC64;  
 Query Match 32.1%; Score 1270.5; DB 1; Length 749;  
 Best Local Similarity 36.1%; Pred. No. 6.9e-78;  
 Matches 273; Conservative 149; Mismatches 290; Indels 45; Gaps 19;

QY 13 KKANGRIALVYVGGLVIGLILFVSQGLSLQAKOE--CYKPECIEAANAALSKV 70  
 Db 18 KKGRWPEPLISLV---LVL--LTVIAVTAIALYATYRDDICKSSPICSAARLIGNM 72  
 QY 71 NLSVDCDNFEPACDGMISNNPREDMPSYGVYEWLRHNOVLKELLESISRRRTE 130  
 Db 73 DATPECTEFKYACGGMKRNVIPETSRYSNFIPLNDELVLKDLQ--PRTEIV 130  
 QY 131 AIOKATIVSSCKNEKAIEKADAPLHLIRSPFRVLESNIGPEGWSE---RRFSL 187  
 Db 131 AVQKATILRSCVNEPAIDSRGGPULKIL--PDYAGWVAATON-----NFOYGTGWSA 183  
 QY 188 LQTLATFRQOYSNVFIRLYSPDDKASNEHLKIDQATISLAVREDYLNSTFAKSRD 247  
 Db 184 EKSIQNLNSNGKRVILNFEVGTDDKSNMNIHIDQPRGLPSR--DIYECTGYEACT 242  
 QY 248 ALYKEMVDTAVL-----IGANSSRAEHDMKSVLRLEIKAEIMIPENPTSE--AMYNK 300  
 Db 243 AYVDEMIAVAKLIRGEELPIDEQISVENKRVLEKEITANNTKSEDNDDMLLYNM 302  
 QY 301 NISELSAM-----PODWLGYIKVYIDRLYPLKDISPENYVVRPOYKDLFRIL 354  
 Db 303 TLAQONNFSLEINGKEPFSMNFETNISTVNI-----NIPNEDVYVAPETILKLPIL 358  
 QY 355 GSERKKTIANLYVMRYSTRIPNLSRROFRMLEFSVIOGTTLLPQWDKVNIESAL 414  
 Db 359 TKYPRDFQNLFSWRFIMDLVSSLSKTYKDSNAEFKALYGTTSSEATWRRCANYNGNM 418  
 QY 415 PYVYKAFVYVYFOEDKKEEMELVSGVWAFIDMLEKENEMDAGTKRAKARAVLA 474  
 Db 419 ENAVGRLYVEAFRAGESKHVEEDLIAQIREVFIQTLID--DLTMADPETKKAEEKLALKE 477  
 QY 475 KVGYP--EFINDTHVNEEDLKAIFSEADYFQVNLQRTKLAOSDFEWMRAKVPKTEPTN 533  
 Db 478 RIGYPDIVSNDKLNNEIYELNLYKDETFENIQLNLFSSOSKOLKRLERVDKDEWITG 537  
 QY 534 PTIVNAFYASTNOIPEPPAGELOKPEFPGTEPRSLSYGALGVYGHFTGPPNNRGKY 593  
 Db 538 AALVNAFYSSGRNQLVFPAGIILPPFF--SAQOSNLNANGIGMVIHGHITTFGFDNGRNF 596  
 QY 594 DKNGNDPMWSTSEEEKFEKTKCMINOYSNYWKA--GLWVKRKLGENIADNGILRE 652  
 Db 597 NKGGDLVDMWTOGSANNFREGSQCMVYQGNFSDWLAGGQHLNINLTGENIADNGIGQ 656  
 QY 653 ARFAYRKWINDRQGLEPPLPGITFTNNQLEFLSYAHVRCNSYRPAREROVIOGAHSP 712  
 Db 657 AYRAVQNTV--KKNG--EKKLPGIDLNKQLFLNFAQVQMGYTRPAYVANSIKTDVHSP 713  
 QY 713 PQFRVNGAISNSEEFQKAFNCPNSTNMRCMDSCRLW 749  
 Db 714 GNFRIIGSLQNSYSESEAFQCPKNSYNN--PEKKCRWV 749  
 RESULT 5  
 NEP\_RAT  
 ID NEP\_RAT STANDARD; PRT; 749 AA.  
 AC P07861;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)  
 GN (Enkephalinase).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid-10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE-87213218; PubMed-355489;  
 RA Maltby B., Schofield P.R., Kuang W.-J., Seeburg P.H., Mason A.J.,  
 RA Henzel W.J.;







[illegible]





FT ETLRESVTLALQMSYKRRATLDEEDLVDSLSGDIYPMG  
(IN ISOFORM D).  
SQ SEQUENCE 762 AA; 86125 MW; D6B8253BC67CCAD8 CRC64;

Query Match 31.4%; Score 1243.5; DB 1; Length 762;  
Best Local Similarity 37.5%; Pred. No. 4.6e-76;  
Matches 277; Conservative 120; Mismatches 284; Indels 49; Gaps 19;

QY 23 LVFVGGTIVLGIITLFLVSGGLSLQAKQCYCLKPECIEAAAILSKVNLSDPCNFR 82  
DB 61 LVVAV-ALTAALVACIALGIGIYRTFRPPVCLTEACVSTSLSDMDPTVDCODEFT 119  
QY 83 FACDGMISNPIDEDMSYGVYPMLRHNDLKLKELLSISRRDTEAIORAKILYSSC 142  
DB 120 YACGGMITKANVPDGSRRGTSNLMENHQAIIKLHLENSTASA--SEAEKRAQYVYRAC 177  
QY 143 MNEKAIEKADAKPLHLIRSPRPVLESNIGPVGSEKRSFSLQTLATRGQYSNV 202  
DB 178 MNETRIELKAKPLMELIEKLK-GWNI-----TGPMKDNFG--DTLQVYVTAHYRTSP 227  
QY 203 FIRLYVSPDKASNEHLKIDQATLSLAVREDYLDNSTEAKSYRDALYKFNVDYAVL-G 261  
DB 228 FFYSYASADKSNNSNVLYQVDSGLPSPRDYLL-NKTENEKVLGYLVYVQGLKLG 286  
QY 262 ANSSRAEHDKSVLRLEIKIAEIMIPHENRTSEAM-YNKMNISLSAMIPQDMGITYK 320  
DB 287 GDEDSIRPQMOQILDEFTALANTITPOEKRBELIYKVAETLAIPALNMLPFLNA 346  
QY 321 VITRILYPLHAKOISBSENVYVPOYFKDLERILSERRKTIANYLVNMYSRIPNLSR 380  
DB 347 I-----FYP--VEINSEPIVYVDEKYLROVSTLINSKCLNNYMMNLVTRKSSFLDQ 400  
QY 381 RFQRYMLFSRVIOGT-TLLPOMDKCVFISALPYVVGKFPVDTYQDEKKEMEELV 439  
DB 401 RFQDADEKFMEMWGTGKICLRKMFQVSDTENNGFALGPEYKATFAEDSKNIAEII 460  
QY 440 EGYRAEFIMLEKENEMDAGTKRKAERAVLAKVGPFFIM-----NDTYHNE 490  
DB 461 LEKKAFFESST-STLKWDEDFRRAKAKADAIYMMIGYPIFMDPELDVFEDYNAV 519  
QY 491 DKAIFSEADYFNVLOTBKRIAQSDFFMLKRAVPEKTEMTNTTNYAFYASTNOIRF 550  
DB 520 DL-----YFENAKMFNFSLVADVDRKAPNDKSMPTPMYNAVYSPKTEIVE 570  
QY 551 PGELOKPEPFGTEYPSLSYGAIGVYGHETFGDNNKGYKGNLDPMWSTSEBK 610  
DB 571 PAGIIQAEFFYRKS--PNAIIFGIGVYGHETLHAFDQGREYDKDNLPMKNSVEA 629  
QY 611 FEKTKMINOYSNYMKKAGLNTKGTGTENTADNGLEAFRAYRKVINDROGLEE 670  
DB 630 FKQTECHAVQOYNNI--SVNGEPVNGRHTIGENTADNGGLKAAVRAVQNNV--KKNGADQ 685  
QY 671 PLLGRTFTNNQFLFLSYAHKNSYRPEARREVOYGAISPOOFIRNGAISSEFOQA 730  
DB 686 -ILPFLIGLISNQLFELFAGQYWCVSRTPESSHGLITDPHSPSRFVIGLSNKEFSEH 744  
QY 731 FNCPPNSTMNGMSCLRM 749  
DB 745 FRCPLGSPMN-PRHKECVW 762

RESULT 10  
ECEL BOVIN  
ID ECEL BOVIN STANDARD; PRT; 754 AA.

AC P42891;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, last sequence update)  
DT 15-JUN-2002 (Rel. 41, last annotation update)  
DE Endothelin-converting enzyme 1 (EC 3.4.24.71) (EC-1).  
GN ECEL.  
OS Bos taurus (Bovine).  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euteria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
RX MEDLINE=95104423; PubMed=7805846;  
RA Schmitt M., Kroeber B., Jacob E., Seuburger H., Subkowski T.,  
RA Otter R., Meyer T., Schmalzing G., Hille H.;  
RT "Molecular characterization of human and bovine endothelin converting  
RL enzyme (EC-1).";  
RL FEBS Lett. 356:238-243(1994).  
CC -1- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1.  
CC -1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-  
CC -1- TRP-1-VAL-22 bond in the precursor.  
CC -1- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- SUBUNIT LOCATION: Type II membrane protein.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL: Z35306; CAA84547.1; -.  
CC HSSP: P08473; IDMT.  
DR MEROPS: M13.002; -.  
DR InterPro: IPR000718; Peptidase\_M13.  
DR InterPro: IPR000130; Zn\_Mrppeptase.  
DR Pfam: PF01431; Peptidase\_M13; 1.  
DR PRINTS: PR00786; NEPRILYSIN.  
DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;  
KW Signal anchor.  
FT DOMAIN 1 52  
FT TRANSMEM 53 73  
FT FT  
FT DOMAIN 74 754  
FT METAL 591 591  
FT ACT SITE 592 592  
FT METAL 595 595  
FT METAL 651 651  
FT ACT SITE 655 655  
FT CARBOHYD 150 150  
FT CARBOHYD 171 171  
FT CARBOHYD 194 194  
FT CARBOHYD 254 254  
FT CARBOHYD 300 300  
FT CARBOHYD 346 346  
FT CARBOHYD 367 367  
FT CARBOHYD 523 523  
FT CARBOHYD 616 616  
FT CARBOHYD 635 635  
SQ SEQUENCE 754 AA; 85616 MW; E9276CCBBE6FF4C CRC64;  
Query Match 31.4%; Score 1241.5; DB 1; Length 754;  
Best Local Similarity 37.9%; Pred. No. 6.2e-76;  
Matches 282; Conservative 120; Mismatches 282; Indels 61; Gaps 21;

QY 23 LVFVGGTIVLGIITLFLVSGGLSLQAKQCYCLKPECIEAAAILSKVNLSDPCNFR 82  
DB 53 LVVAV-ALTAALVACIALGIGIYRTFRPPVCLTEACVSTSLSDMDPTVDCODEFT 111  
QY 83 FACDGMISNPIDEDMSYGVYPMLRHNDLKLKELLSISRRDTEAIORAKILYSSC 142  
DB 112 YACGGMITKANVPDGSRRGTSNLMENHQAIIKLHLENSTASA--SVSEAEKRAQYVYRAC 169  
QY 143 MNEKAIEKADAKPLHLIRSPRPVLESNIGPVGSEKRSFSLQTLATRGQYSNV 202  
DB 170 MNETRIELKAKPLMELIEKLK-GWNI-----TGPMKDNFG--DTLQVYVTAHYRTSP 219



Db 236 DNF--MEVLAAGVATYRATPEFYIVISADSSNSNIYQDQGLPLPSRDYLL-NRTAN 292  
 Qy 243 KSYRDALYKFWYDVAVLGANSRAEDMKSVLRLEIKIAELMIPH-ENKTSAMYNKAN 301  
 Db 293 EKVLTAYLIDMEELGMLGGRPTSTREDOQVLELEIOLANTIVPODQREDEKIKHKMS 352  
 Qy 302 ISELISAMIPOFMDLGYIKKVIIDTRILYPHLKDIPSPNVVVRPOYKDKLFRILGSEKKT 361  
 Db 353 ISELQALAPSDMDLEFLISFLSP-----LELSDSEPVVYVGYMDYLOQVSELINTEPSI 406  
 Qy 362 IANLVWRYMYSRIPNLSRPFQRYLWLEFSRVIOGT-TLLLPQMDKCVNFIESALPYVYGK 420  
 Db 407 LANLILNVLQYKTTSLDRFESAOEKLLETTETKSKSCVPMQOCISNTDQALFALGS 466  
 Qy 421 MFVDVYFQEDKKEMELVEGVWAFIDMLEKENEMAGSTRKAKKARAVLAVGYTPE 480  
 Db 467 LFKATFEDROSKKEIAGMISEIRTAEEAL-GQLYWMDKTRQAKKEADAIYMDIGFDP 525  
 Qy 481 FIMNDTHVNDLKAIFESADYFGVNLQTRKYLAQSDPEFWLKRKAVPKTEMTNPTVNAF 540  
 Db 526 FILEPEKEDVDYDGEISDSFQNMMLYNFSAKVMAQDQLRKPPSRDQMTPOYVNAF 585  
 Qy 541 YSASTNOIRFPAGELQKPFPMGTETPSYCAIGVYIGHETGFDNNKGRKNGND 600  
 Db 586 YLPTKNEIYFPAIGLIQAPFY-ARNHKKALNFGGIGVWGHETLTAIFDQGEYDKGNLR 644  
 Qy 601 PMWSTSEKKEKTKKCHINOYSYKKAQNLNKKRTLGENTADNGSLREAFRAYRY 660  
 Db 645 PMWQESLAAEFNHTACCEEDYNDY--QVNGERLNGRTGTGENTADNGSLREAFRAYRY 702  
 Qy 661 INDRQGLEEPLLPGITPTNNQLEFISYAHYCSYRPEARREVOYGASPPQFRYNGA 720  
 Db 703 L--RKHG--EQOQLPVGGLTNQLPFGVGAOVWCVSRPESHSBELVTPDPSPARFVLTG 759  
 Qy 721 ISNSEFOKATNCPNSTMNGMDSCKLM 749  
 Db 760 LSNKDFLHFGCEVSPMNG-QLCFVW 787

## RESULT 12

ECE2\_BOVIN

STANDARD;

PRT; 787 AA.

AC 010711;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).  
 GN ECE2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxId=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95318093; PubMed=7797512;  
 RA Emoto N., Yanagisawa M.;  
 RT "Endothelin-converting enzyme-2 is a membrane-bound, phosphoramidon-  
 sensitive metalloprotease with acidic pH optimum.";  
 RL J. Biol. Chem. 270:15262-15268(1995).  
 CC 1- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1. OPTIMUM PH IS  
 CC 5.5. INACTIVE AT NEUTRAL PH.  
 CC 1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-  
 CC Trp-1-Val-22 bond in the precursor.  
 CC 1- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.  
 CC 1- SUBCELLULAR LOCATION: INHIBITED BY PHOSPHORAMIDON.  
 CC 1- SIMILARITY: BELONGS TO TYPE II membrane protein.  
 CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
 CC -----  
 Db EMBL: U27341; AAA82927.1;  
 Dr HSSP: P08473; 1DMT.  
 Dr MEROPS: M13.003;  
 Dr InterPro: IPR000718; Peptidase\_M13.  
 Dr InterPro: IPR000130; Zn\_MTPeptidase.  
 Dr Pfam: PF01431; Peptidase\_M13; 1.  
 Dr PRINTS: PR00786; NEPRILysin.  
 Dr PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 Dr HydroLase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;  
 Dr Signal-anchor.  
 FT DOMAIN 1 82  
 FT TRANSMEM 83 103  
 FT METAL 104 787  
 FT ACT\_SITE 624 624  
 FT METAL 625 625  
 FT METAL 628 628  
 FT ACT\_SITE 684 684  
 FT CARBOHYD 164 164  
 FT CARBOHYD 183 183  
 FT CARBOHYD 187 187  
 FT CARBOHYD 228 228  
 FT CARBOHYD 288 288  
 FT CARBOHYD 333 333  
 FT CARBOHYD 400 400  
 FT CARBOHYD 456 556  
 FT CARBOHYD 549 649  
 FT CARBOHYD 657 657  
 SQ SEQUENCE 787 AA; 88957 MW; F085C2921DAF0BF2 CR664;

## Query Match

29.9%

Score 1184; DB 1;

Length 787;

Best Local Similarity 35.1%;

Pred. No. 4.9e-72;

Matches 265; Conservative 138; Mismatches 313; Indels 38; Gaps 18;

Qy 4 ETGSGVETGKANKGRIRALVFGGTLVLTILF--LYSQGL-LSLQAKQCYCKPKPCI 60  
 Db 64 EAGFRKTSRLGLHLOLELVL-AGVSLALLGLGVALGQVHRPDSHTCTEACI 122  
 Qy 61 EAAAILSKVNLVSDQDNFERRACDQWISNPIDNPSTYVFWLRRHNDLKLKELLE 120  
 Db 123 RVAGKILLESIDRVSCEDPQPSGCGWTRNPLDQGSRRMNSNSLMDQALIKHLE 182  
 Qy 121 KSISSRDTEALQAKIILYSSCMNEKATEKADAKPLHLRSPRMVYLESNTG---PE 177  
 Db 183 NT-TFNSSSEAEKQRFYLSCLQVERIEELGA-----HALD-----LDKIGNNVT 230  
 Qy 178 GVWSEKRFSLQTLATFRQOYNSVFIILYSPDDKASNEHILKIDATLSLAVREYLD 237  
 Db 231 GPWDDQNF--MEVLAAGVATYRATPEFYIVASDKSSNSNIYQDQGLPLPSRDYLL- 287  
 Qy 238 NSTEAKSYDALYKEMVDVAVLGANSRAEDMKSVLRLEIKIAELMIPH-ENKTSAM 296  
 Db 288 NNTAEKVLTAVIDYMEELGMLGGPSTREQROYLELEIOLANTIVPODQREDEK 347  
 Qy 297 YKKNMISELSAMIPQFMDLGIKVIIDTRILYPHLKDIPSPNVVVRPOYKDKLFRIL 356  
 Db 348 YHKMSIAELQALPSMDLEFLISFLSP-----LELSDSEPVVYVGYMDYLOQVSELIN 401  
 Qy 357 EKKTIANYLVWRYSRIPNLSRPFQRYLWLEFSRVIOGT-TLLLPQMDKCVNFIESALP 415  
 Db 402 TEPVLYNNYLIWNLVQTTSLDRFESAOEKLLETTETKSKSCVPMQOCISNTDQAL 461  
 Qy 416 YVVGMPVDYFQEDKKEMELVEGVWAFIDMLEKENEMAGSTRKAKKARAVLAK 475  
 Db 462 FALSLVYKATFDRQSKKEIAGMISEIRVAFEEAL-GHYWMDKTRQAKKRAALIIDM 520  
 Qy 476 VGPEFTINDTHVNDLKAIFESADYFGVNLQTRKYLAQSDPEFWLKRKAVPKTEMTNPT 535

Db 521 IGFPELLEPEKELDDVDYGVSEDSFFQNMNLNYSNAKVMADOLRKPSPSDMSMTQ 580  
 QY 536 YVNAFSASTNOIRPAGELQKPEFWGTEPRISYALIVYGHETHEGDNNGKRYDK 595  
 581 YVNAFSASTNOIRPAGELQKPEFWGTEPRISYALIVYGHETHEGDNNGKRYDK 639  
 QY 596 NGMLDWMSSTSESEKPEKTEKCMINQSYNWKRAGLVWKRTLGENDANGLEARE 655  
 640 EGNLIRFWMWNESLAIFRNTACIEFOYSOY--QVNGEKLNROTLGENDANGLEARE 697  
 QY 656 AYKRWINDRROGLEPILGTFITNNQLEFLSYAHRCNSYRPPARROVIGASHSPDF 715  
 698 AYKRWINDRROGLEPILGTFITNNQLEFLSYAHRCNSYRPPARROVIGASHSPDF 754  
 QY 716 RVNGAISNSEFOKAFNCPCPNSTNMGKMDSCRLM 749  
 755 RVNGAISNSEFOKAFNCPCPNSTNMGKMDSCRLM 787

RESULT 13  
 ECEL\_MOUSE STANDARD; PRT; 775 AA.

AD ECEL\_MOUSE Q9JMI0: 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein)  
 DE (Damage-induced neuronal endopeptidase).  
 GN ECEL OR XCE OR DINE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20226106; PubMed=10759559;  
 RA KIRYU-Seo S., Sasaki M., Yokohama H., Nakagomi S., Hirayama T.,  
 RA Aoki S., Wada K., Kiyama H.;  
 RT "Damage-induced neuronal endopeptidase (DINE) is a unique  
 RT metalloproteinase expressed in response to neuronal damage and  
 RT activates superoxide scavengers".  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:4345-4350(2000).  
 CC -1- FUNCTION: May contribute to the degradation of peptide hormones  
 CC and be involved in the inactivation of neuronal peptides.  
 CC -1- COFACTOR: Binds 1 zinc ion (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AB026294; BAA95005.1;  
 CC HSSP: P08473; IDMT.  
 DR MEROPS: M13.007;  
 DR MGD: MGI:1343461; Ecel1.  
 DR InterPro: IPR000718; Peptidase\_M13.  
 DR InterPro: IPR000130; Zn\_MTPeptide.  
 DR Pfam: PF01431; Peptidase\_M13; 1.  
 DR PRINTS: PRO0786; NEPRILysin.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 DR GlycoSite: 1; ZINC; PROTEASE; Metal-binding; Zinc;  
 KW Glycoprotein; Transmembrane; Signal-anchor.  
 FT DOMAIN 1 61  
 FT TRANSMEM 62 82  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT LUMENAL (POTENTIAL).  
 FT METAL 612 612  
 FT ZINC (CATALYTIC) (BY SIMILARITY).

ACT SITE 613 613 BY SIMILARITY.  
 METAL 616 616 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 672 672 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 656 656 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 775 AA; 87993 MW; 5344595D/C534B9 CRC64;  
 Query Match 25.1%; Score 992; DB 1; Length 775;  
 Best Local Similarity 30.7%; Pred. No. 3.9e-59;  
 Matches 241; Conservative 159; Mismatches 290; Indels 94; Gaps 22;

QY 11 TGRKANRGTAL-----VVFVGTLYGLTILFVSGLLSLQ-----AKQ 52  
 41 SGRSAS-GSRGSLPRMRNREVCLLSG-LVPAIGALAILAAMALKTLGPAAGGACPE 98  
 QY 53 YCLKEPCIEAAILLS-KVNLSDVPCNFRPCDGMISNPIPEDMPSYGYPMILRHNV 111  
 99 GCPERKAFARARFSLNADASIDPCDFYSFGCGMLRHRAIPDCKLGTGTAIGEON 158  
 QY 112 DLKKELEKSISRRTD-----EALQKALYSSCKNEKAIEKADAKPLHILRSPR 166  
 159 EERLRRL-----ARPTGPGGAQRKVRAPFRSCIDMRLEIRGPRMLEVTEDC--- 209  
 QY 167 WPLIESNIGPEGW-----SERKSLQTLATPRGYSNSVETRLVYSPDKASNE 217  
 210 -----GGWDLGAGNADRPGAARDNLNLYKAGYSAALSLTSLIDDRSSR 258  
 QY 218 HILKLOATSLAVRDYDNDNSTEAKSYDALYKEMVDVAVLLGANSRREHDKSVLRL 277  
 259 YVRIIDGGLTLERLTYLAQDESEKILAAAYVEMORILLGADA--VQKQELTQL 316  
 QY 278 EIKTAEIPIHEN---RTSEAMTKMNISELSAMIPQDMGLYIKVYIDRLYHLKDIS 334  
 317 EORLANISVEEYDLRDVSSATNKVTLQLOKIIPIHQLMKLQIDP-----EDFS 369  
 QY 335 PSENVVVRVPOFKDLRIILGSRKRTIANYLVKMYSTRIPNLSRPOYMLERSVIQ 394  
 370 EEEVYVLATDYMQVYQLRTPRRIHNYLVWRVAVVLSHLSPREALHELAEME 429  
 QY 395 GTTILLPQMDK-----CVNFIESALPYVVGKMFVDYFOEDKEMMEELVEGYRAFI 447  
 430 GN-----DKPOLARVYCLQANRHMALGALFHEHSAKSKAKVOQLVEDIKYILG 482  
 QY 448 DLEKENEMDAGTRKAKKERARVLAQVPEFIANDTVNDLKALFESEADIFGVNL 507  
 483 QRLP-ELDMMDAQTFARAKLQYMAVWYGPDLKPEAVDKYE-PEVHEKTYKNIL 540  
 QY 508 QTRKYLAQDFWLLKAVPKTEMTNPTVNAFYSASTNOIRPAGELQKPEFWGTEPR 567  
 541 NSIRFSTQLSVKRIQEVDSKSWLLPQALNAVLLPKNGVYVYAGILQ-PLTYLDPDFQ 599  
 QY 568 SLISYAGIVYGHETHEGDNNGKRYDKNGNLDPWMSSESEKPEKTEKCMINQSYN 625  
 600 SLVYGGIGTILGHEHLYGDDWGCQYDRSGNLIHMTASTSRLLHAECIVRLYDNFY 659  
 QY 626 YMKKAGLVNGKRTLENDANGLEAREFRAYRWINDRROGLEPILGTFITNNQLE 665  
 660 YNCR-----VNGKRTLENDANGLEAREFRAYRWINDRROGLEPILGTFITNNQLE 712  
 QY 686 LSYAHVRCNSYRPPARROVIGASHSPDFRYNGAISNSEFOKAFNCPCPNSTNMGDS 745  
 713 IAPQNMCKIRRSQSYLYVLTLDKHAPEHYRVLYGSVQFEERGRAFHCPKXSPNN-PVHK 771  
 QY 746 CRLW 749  
 772 CSYW 775

RESULT 14  
 ECEL\_MOUSE STANDARD; PRT; 775 AA.  
 ID ECEL\_MOUSE Q9JHJ3: 092192;  
 AC

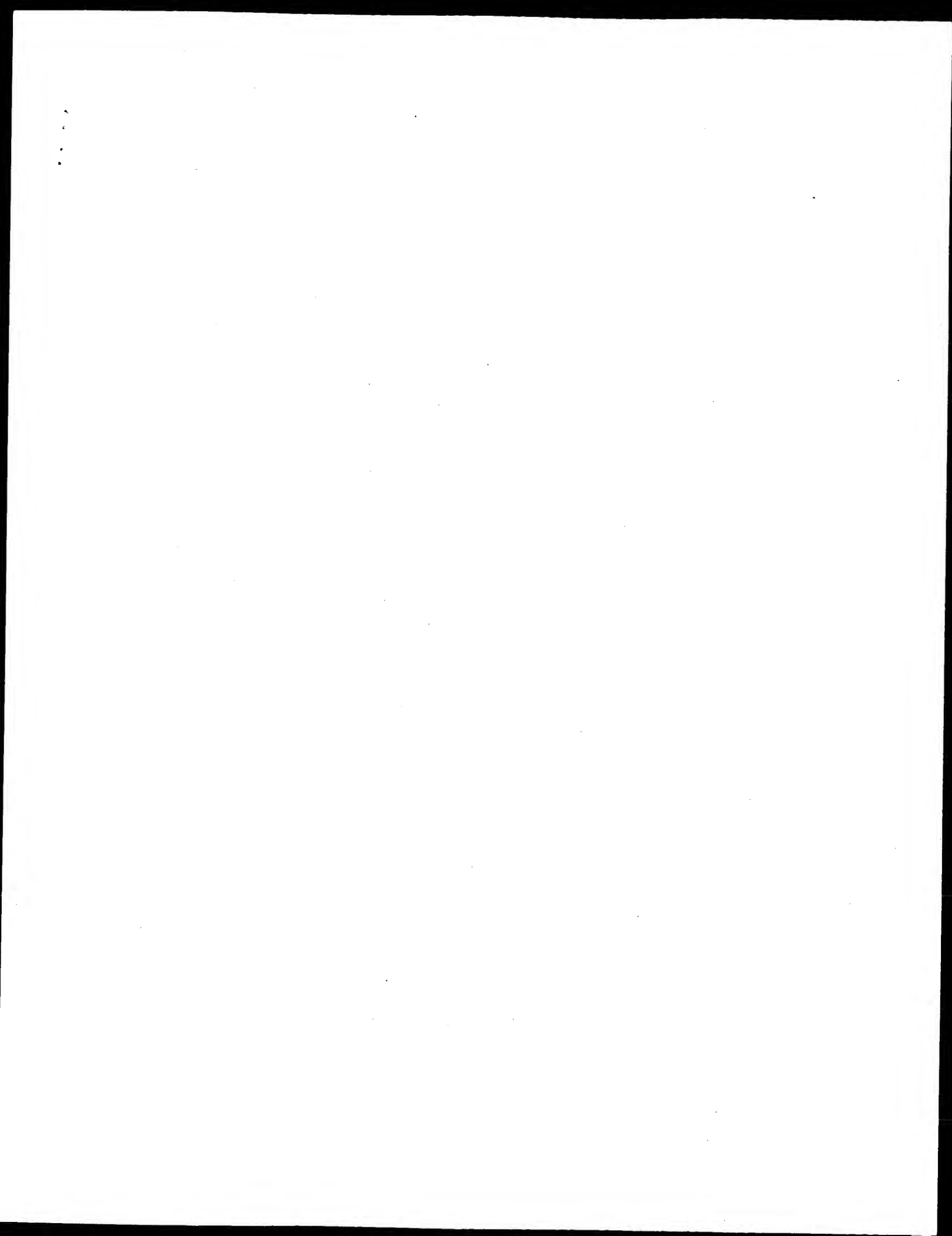
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SEQ	SEQUENCE	775 AA:	87944 MW:	0823091P89A41556 CAC64;
Query Match		24.7%:	Score 977:	DB 1: Length 775:
Best Local Similarity		30.5%:	Pred. No. 4e-58:	
Matches 239:		Conservative 158:	Mismatches 293:	Indels 94: Gaps 22:
QY	11	TGKKANRGRRL-----VFVGGTLVLGTLFLVSGQLSLQ-----AKOE	52	
DB	41	SGRSAS-GAKSLPFWNRREVCLLSG-LVFAAGLCALIAALAKLYGPAAGATGGACPE	98	
QY	53	YLCKEPCIEFAAAILL-KVNLVSDPCDFEFAADGHIISNNIPEDMPSGYVWYRHNY	111	
DB	99	CGPEKAPARARAFSLANLADISIDPCQDFSEACGGVLRHRAIPDKLTGTIAAIGEQN	158	
QY	112	DLKLELEKESISRROD-----EAIKAKILVSSCMNEKAIEKADAPKLHLIRASPR	166	
DB	159	EBRLRRL-----ARPTGPGGAQAQKVAFAFRSCLDMEIRLDRPRMLVIEEC---	209	
QY	167	WPLVESINIGPEGW-----SERKFSLOTLAFRGQVSIVYRLVSPDDKASNE	217	
DB	210	-----GGMDLGGADRGADRGARMDLNRLLYLAQGYISAALEFSLTSLDRNRSR	258	
QY	218	HLKLDQATSLAVBEDYLDNSTEASRYDALYKKNVADTAVLIGANSSRAEHDMKSVRL	277	
DB	259	YVIRIDQGLTLPERTLTYLAODEGSKVLAARKVMERLRLRLGADA--VEGKQELIQL	316	
QY	278	EIIAELMIDHEN--RTSEAMYNKNINSELSAMTPOFDMGLKGVYIKKYVDTLTYHLADIS	334	
DB	317	EQRANLISSEVDLRRDVSYYNKKVTIGQLKIRPHLQMKLLDQIQ-----BDFS	369	
QY	335	PSENVVVRVPOYFKDLFRILGSEKKTLANTLYRMAYVSRPLNLSRRQYRWLEFSRVIQ	394	
DB	370	EEFEVVLATIDYMQVSLIRSTRILANTLYMVEVVVLESHLSPFEALHELAKEME	429	
QY	395	GTTTLIPQDK-----CVNFIESALPYVKKAFVNVYFOEDKEMHELVGYSKRAFI	447	
DB	430	GN-----DKPOLARVLCQANRHFGMALGALFVHEHSSASKAVVQDLVDIYIIG	482	
QY	448	DMLKENEMDAGTRKRAKERAVALKVGCPETINDYVNEDLAKIKFSEADYGVNVL	507	
DB	483	QRL-EELMDMDAQKKAARAKLYMMAMVGPDPDLKPEAVDEYE-FEVHEKTYLTKL	540	
QY	508	QTRKLAGSDPFMLRKAVPTKTEFTNTVNAEYSASTNOIRPEAOELCPFWMGVEYR	567	
DB	541	NSIFPSIOLSVKTKROEVDSKTWLLPFOALNAVYLLPNKNQWMPFACILO-PLTYRDPDQ	599	
QY	568	SLSYGAIGTVIGHETFGFDNNGRKYDKNGNLDPWMSSTSEKFEKTKCMINQSYN--	625	
DB	600	SLANGGIGITIGHEILFTGVDYDMCGQYLDKRGNLLHMTWTEASYSRFLHKAECYRLADNFTV	659	
QY	626	YMKKAGLVNKGKTLGENTADNGLGLEAFRAYKRWINDROGLEPPLGTLFFNNOLF	685	
DB	660	YNOR-----VNGKHTLGEENTADMGGLKLAAYAYQKWV--REHGPBHR-LHRKTYHNOLEF	712	
QY	686	LSTAAHRCNSYRPEARAEQYGAISPPQGFNRNGALINSSEQFAFNCPSPNSTNRGMS	745	
DB	713	IAFNQMCIKRRSSQSYIQLVLTDKNAPEHYKLVSSQFEFGAFAFCPKDSPWN-PVHK	771	
QY	746	CRLM 749		
DB	772	CSWV 775		



OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Caudate, and Spinal cord;  
 RX MEDLINE=99132387; PubMed=9931490;  
 RA Valdenaire O., Richards J.G., Faull R.L.M., Schweizer A.;  
 RT "XCE, a new member of the endothelin-converting enzyme and neutral  
 RT endopeptidase family, is preferentially expressed in the CNS.";  
 RL Brain Res. Mol. Brain Res. 64:211-221(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20164043; PubMed=10698686;  
 RA Valdenaire O., Rohrbacher E., Langeveld A., Schweizer A., Meijers C.;  
 RT "Organization and chromosomal localization of the human ECE1 (XCE)  
 RT gene encoding a zinc metallopeptidase involved in the nervous control  
 RT of respiration.";  
 RL Biochem. J. 346:611-616(2000).  
 CC -1- FUNCTION: May contribute to the degradation of peptide hormones  
 CC and be involved in the inactivation of neuronal peptides.  
 CC -1- COFACTOR: Binds 1 zinc ion (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the CNS, in particular in  
 CC putamen, spinal cord, medulla and subthalamic nucleus. A strong  
 CC signal was also detected in uterine subepithelial cells and around  
 CC renal blood vessels. Detected at lower levels in amygdala,  
 CC caudate, thalamus, pancreas and skeletal muscle. Detected at very  
 CC low levels in substantia nigra, cerebellum, cortex, corpus  
 CC callosum and hippocampus.  
 CC -1- PTM: N-glycosylated.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.  
 CC -----  
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 CC -----  
 DR EMBL: Y16187; CAA76113.1; .  
 DR EMBL: AJ130734; CAB86601.1; .  
 DR HSSP: P08473; IDMT.  
 DR MEROPS: M13.007; .  
 DR Genew: HGNC:3147; ECE1.  
 DR MIM: 605896; .  
 DR InterPro: IPR000718; Peptidase\_M13.  
 DR InterPro: IPR001230; Prenyl\_site.  
 DR InterPro: IPR000130; Zn\_MTPeptide.  
 DR Pfam: PF01431; Peptidase\_M13; 1.  
 DR PRINTS: PR00786; NEPRILYSIN.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 DR HydroLase: Protease; Metalloprotease; Metal-binding; zinc;  
 KW Glycoprotein; Transmembrane; Signal-anchor; Polymorphism.  
 KM HydroLase: Protease; Metalloprotease; Metal-binding; zinc;  
 FT DOMAIN 1 59  
 FT TRANSMEM 60 82  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT LUMENAL (POTENTIAL).  
 FT ZINC (CATALYTIC) (BY SIMILARITY).  
 FT BY SIMILARITY.  
 FT ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ZINC (CATALYTIC) (BY SIMILARITY).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT H -> O (IN DBSNP:2741281).  
 FT /FTID=VAR\_012813.  
 FT Y -> H (IN DBSNP:1529874).  
 FT /FTID=VAR\_012814.  
 FT V -> I (IN REF. 2).  
 FT VL -> AF (IN REF. 2).  
 FT CONFLICT 286 286  
 FT CONFLICT 757 758

FT CONFLICT 763 763 V -> D (IN REF. 2).  
 SQ SEQUENCE 775 AA; 87781 MW; 5B43E0F11C5B55C CRC64;  
 Query Match 24.58; Score 969.5; DB 1; Length 775;  
 Best Local Similarity 30.7%; Pred. No. 1.3e-57;  
 Matches 231; Conservative 157; Mismatches 297; Indels 67; Gaps 19;  
 QY 23 LVPVGGTLVLTLLFVSGGLSL--QAKOYCLKEPCEIEAAAIL-SKYNLSVDPEDN 79  
 DB 66 LVFAAGCAILLAMALTYLGPVAAAGGACGCEGPEKAFARARFLAANLADSIDPCOD 125  
 QY 80 FEFACDGMISNNPIEDMPSYGVYPMWLNHVDLKLLEKLSISRRDTEALOKATLY 139  
 DB 126 FYFACGGWLRHAIIPDDKLTYGTALIGOEERLRLARP-GGGPGGAQRVAF 184  
 QY 140 SSCMKEKIEKADAPLHLIRHSFRFPVLESNIGPGVY-----SER-----KFSILQ 189  
 DB 185 RSLDMREIERLGRPMLEVEDC-----GGMDLGAEFRPVAARWDLNR 230  
 QY 190 TATPFGQYSNVEFRLYVSPDDKASNEHLKLDQATLSLAVREDYLDNSTEAKSYDAL 249  
 DB 231 LLKKAQGYSAALSLVYSDDRSSRVYRIDQGLTEPRLTYLAQDDSEKVLAAV 290  
 QY 250 YFPMVDVAVLANSRAHDKSVLRLEIKAEIMIHEN---RTSAMNKNMISLS 306  
 DB 291 RYFMERVLSLIGADA--VEQKAQELLOEQALNTVSEYDRLRDVSMYNTKYLQLO 348  
 QY 307 AMIPQDMVYIKKYIDRTLYPHLKDIPSENVVYVQVQEDPRLIGSEKRTIANYL 366  
 DB 349 KITPHLRKMWLDQIFQ-----EDFSEEEVLLATDYMQVQSILRSTPHRYLNYL 401  
 QY 367 VWRVYSRIPNLSRRFQYMWLEFSRYIGTITLLQWOK-----CYNFIESALPYVG 419  
 DB 402 VWRVYVLSSEHSPFERALHELAQEMGS-----DKPOLANVCYQANRHEGMAIG 454  
 QY 420 KMPVDYVPEQDKKEMEEELVEGVRAFDLMEKEMMDAGTKRKAKERARAVLAKVGP 479  
 DB 455 ALVHHFHSASAKAQQLVEDIKYLGRLR-ELDDMDAERRAARAKLYMMVAVGVP 513  
 QY 480 EFTMNDTHVNEDLKAIFSEADYFGVNIQTRKYLAOSDFWLRKAVPKTEWNTNPTVVA 539  
 DB 514 DFLKPDADVDEYE-FEVHEKTYFKNLIINSIRFSIOLSVYKIRQEDVKSTWLLPQALNA 572  
 QY 540 FYGASINQIRFPAQELQKPFQWTEYPRSLSYGALGIVYGHETFGDNGGRKYDKGNL 599  
 DB 573 YLPPNKNQVFPAGILO-PTLYDPDPQSLNGGIGITIIHGHETFGYDWMGGOYDRSGNL 631  
 QY 600 DPMWSTSEKFEKTKCMINQYSNY--YWKAGLVNKKRRLGENTIADNGILREAFRAY 657  
 DB 632 LHMWTEASYRFLRKACIVRLVDNFTVYNQR---VNGKHITGENIADMGKIKLAYHAY 687  
 QY 658 RKMINDRQGLLEPPLPGITFTNNQLFELSYAHVRNSYRPEARAOVYIGASHPQGFV 717  
 DB 688 QKWV--REHGPENP-LRLKTYTHQLEFLAFAONWCCKRRSSQSIYIYVLTLDKHAHPHYAV 744  
 QY 718 NGAISNSEFOKAFNCPPNSTNNRGMDSCRLL 749  
 DB 745 LGSYSQFEERGVYACPKYSPMNA-HKCSYV 775

Search completed: May 21, 2003, 18:48:18  
 Job time : 31 secs



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OM protein - protein search, using sw model

Run on: May 21, 2003, 18:44:34 ; Search time 41 Seconds  
(Without alignments)  
3764.129 Million cell updates/sec

Title: US-09-913-955A-1  
Perfect score: 3958  
Sequence: 1 MEATGSSVETGKKANRGR.....AFNCPNSTNRMGMSCLRW 749

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :

1: SP.TREMBL.21.\*  
2: SP.Archea.\*  
3: SP.Dactylia.\*  
4: SP.Fungi.\*  
5: SP.Human.\*  
6: SP.Invertebrate.\*  
7: SP.Mammal.\*  
8: SP.Mhc.\*  
9: SP.Organeller.\*  
10: SP.Phage.\*  
11: SP.Plant.\*  
12: SP.Rodent.\*  
13: SP.Virus.\*  
14: SP.Vertebrate.\*  
15: SP.Unclassified.\*  
16: SP.Virus.\*  
17: SP.Dactylia.\*  
18: SP.Archea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3819	96.5	749	11 035812	035812 rat1us nov
2	1380	34.9	742	11 09ERK3	09ERK3 mus musculu
3	1375.5	34.8	765	11 09JUL13	09JUL13 mus musculu
4	1373	34.7	742	11 09QZV6	09QZV6 mus musculu
5	1368.5	34.6	765	11 09QZV7	09QZV7 mus musculu
6	1361.5	34.4	779	11 09ERK2	09ERK2 mus musculu
7	1335	33.7	770	13 093394	093394 perca flav
8	1332.5	33.7	770	4 096PH9	096PH9 homo sapien
9	1257	31.8	752	13 09DGM6	09DGM6 gallus gall
10	1253.5	31.7	758	6 028868	028868 bos taurus
11	1248.5	31.5	758	6 028010	028010 bos taurus
12	1223	30.9	787	5 09DA44	09DA44 adplysia cal
13	1219	30.8	772	5 09BLH1	09BLH1 bombyx mori
14	1209	30.5	848	5 016796	016796 caenorhabdi
15	1208	30.5	763	11 092376	092376 mus musculu
16	1205.5	30.5	661	5 09W435	09W435 drosophila

17	1187.5	30.0	1040	5 08T062	08T062 drosophila
18	1182	29.9	770	5 09UP2	09UP2 hydra atten
19	1153.5	29.1	786	5 08SM51	08SM51 drosophila
20	1150.5	29.1	726	5 09W570	09W570 drosophila
21	1134.5	28.7	736	5 04A857	04A857 caenorhabdi
22	1119	28.3	763	5 09X201	09X201 drosophila
23	1117.5	28.2	739	5 08T660	08T660 venturia ca
24	1014.5	28.6	766	5 018673	018673 caenorhabdi
25	911	23.0	677	5 091774	091774 drosophila
26	822	20.8	665	17 08TPB2	08TPB2 methanosarc
27	814.5	20.6	706	16 09A202	09A202 caulobacter
28	798	20.2	689	2 050642	050642 porphyromon
29	778	19.7	754	5 019831	019831 caenorhabdi
30	691	17.5	167	13 093586	093586 gallus gall
31	672	17.0	663	16 053649	053649 mycobacteri
32	668	16.9	700	16 09P71	09P71 xylella fas
33	653.5	16.5	683	5 09Y136	09Y136 drosophila
34	646.5	16.3	667	16 006075	006075 mycobacteri
35	643.5	16.3	700	5 09VAY0	09VAY0 drosophila
36	607	15.3	717	5 045569	045569 caenorhabdi
37	606	15.3	756	5 08WSK6	08WSK6 dermatocent
38	588.5	14.9	713	11 09E0R2	09E0R2 mus musculu
39	586	14.8	870	5 09CR16	09CR16 ancylostoma
40	584	14.8	870	5 08YTS9	08YTS9 lactobacilli
41	571	14.4	648	5 022763	022763 caenorhabdi
42	567	14.3	798	5 09VAS4	09VAS4 drosophila
43	561.5	14.2	823	5 045131	045131 haemophilus
44	558.5	14.1	823	5 09G7J5	09G7J5 ancylostoma
45	554	14.0	507	5 09G7J5	09G7J5 ancylostoma

## ALIGNMENTS

### RESULT 1

035812 PRELIMINARY; PRT; 749 AA.

ID 035812  
AC 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE PHEX protein.

GN PHEX.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=INCISOR;  
RA MEDLINE=97343325; PubMed=9199930;  
RA Francis F., Strom T.M., Hennig S., Boeddrich A., Lorenz B.,  
RA Brandau O., Mohlke K.L., Cagnoli M., Steffens C., Klages S.,  
RA Borzym K., Pohl T., Oudet C., Econs M.J., Rowe P.S., Reinhardt R.,  
RA Meltinger T., Lehnach H.;  
RT "Genomic organization of the human PEX gene mutated in X-linked  
RT dominant hypophosphatemic rickets.";

KL Genome Res 7:573-585(1997).  
EMBL: A001637; CAA04890.1;  
DR HSP; P08473; IDMT.  
DR MEROPS; M13.091; -;  
DR InterPro: IPR000718; Peptidase\_M13.  
DR InterPro: IPR001230; Prenyl\_site.  
DR InterPro: IPR00130; Zn\_MTPpepase.  
DR Pfam: PF01431; Peptidase\_M13; 1.

DR PRINTS; PR00786; NEPRILASIN.  
DR PROSITE; PS00294; PRENYLATION; UNKNOWN\_1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
SQ SEQUENCE 749 AA; 86305 MW; 690B8E82609C1A63 CRC64;

Query Match 96.5%; Score 3819; DB 11; Length 749;  
Best Local Similarity 95.3%; Pred. No. 3.1e-256;  
Matches 714; Conservative 22; Mismatches 13; Indels 0; Gaps 0;

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QY 1 MEATGSSVETGKANKGRTRIALVFWGGVITLFLVSGGLSLQAKOECYCKPCCI 60
DB 1 MEADAGSTMTGKNGRIRIALALITITGLVGLTLFLVSGGLSFAKOECYCKPCCI 60
QY 61 EAAAIATSKVNLVSDPCDNFEPFACDGTWISNNPDEMPSYGVYPMLRHNDLKTLELLE 120
DB 61 EAAAIATSKVNLVSDPCDNFEPFACDGTWISNNPDEMPSYGVYPMLRHNDLKTLELLE 120
QY 121 KTSIRRRDEALQAKITKSSCNEKATIKAKAPLHLRLHSPPRMVLESNIGPEGVW 180
DB 121 KYSRRRDEAVQAKIITKSSCNEKATIKAKAPLHLRLHSPPRMVLESNIGPEGVW 180
QY 181 SEKESLDTLATFRGOYSNSVFIILYVSPDDKASNEHILKIDQATISLAVREDYLDNST 240
DB 181 SEKESLDTLATFRGOYSNSVFIILYVSPDDKASNEHILKIDQATISLAVREDYLDNST 240
QY 241 EAKSYDALTAKFMPVPAVLILGANSRAHDKSVYRLKIAETIMIPHENTSEAMTKM 300
DB 241 EAKSYDALTAKFMPVPAVLILGANSRAHDKSVYRLKIAETIMIPHENTSEAMTKM 300
QY 301 NISELSAMIPDFMLGYIKVYIDTRYLPHLKDISENVVAVVQYFKDLFRILIGSRKK 360
DB 301 NISELSAMIPDFMLGYIKVYIDTRYLPHLKDISENVVAVVQYFKDLFRILIGSRKK 360
QY 361 TIANTLVNMYYSRIPIINSRPOYHLEFSRYIGTITLLPQWDKCVNFTESALPYVVGK 420
DB 361 TIANTLVNMYYSRIPIINSRPOYHLEFSRYIGTITLLPQWDKCVNFTESALPYVVGK 420
QY 421 MEVDVYFQEDKKEMMELVEGVNAFIDMLEKENEMDAGTKRKAKARAVLAKYCYPE 480
DB 421 MEVDVYFQEDKKEMMELVEGVNAFIDMLEKENEMDAGTKRKAKARAVLAKYCYPE 480
QY 481 FIMNDTYNEDLKIKSEADYEGNVLOTRTYLAQSDPEFLKRAVKTETFTPTVNAF 540
DB 481 FIMNDTYNEDLKIKSEADYEGNVLOTRTYLAQSDPEFLKRAVKTETFTPTVNAF 540
QY 541 YSASTNOIRFAPAGELQKPFMGTEYPRSLSYGAIYVGEHFTGHDNGRKKDKNGND 600
DB 541 YSASTNOIRFAPAGELQKPFMGTEYPRSLSYGAIYVGEHFTGHDNGRKKDKNGND 600
QY 601 PWSSTESSEKFEKTKCMINQYSYVYKKAAGLVKGRITGENIADNGILREAFRAYRK 660
DB 601 PWSSTESSEKFEKTKCMINQYSYVYKKAAGLVKGRITGENIADNGILREAFRAYRK 660
QY 661 INDRQGLEBLLPGITFTNNOLFSLYAHVRCNSYRPEARQVOIGAHSPQORVNGA 720
DB 661 INDRQGLEBLLPGITFTNNOLFSLYAHVRCNSYRPEARQVOIGAHSPQORVNGA 720
QY 721 ISNEEFQAKFNPSTANRKGDCRLW 749
DB 721 ISNEEFQAKFNPSTANRKGDCRLW 749

```

## RESULT 2

```

QYERK3 PRELIMINARY: PRT: 742 AA.
ID QYERK3:
AC QYERK3:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Neprilysin-like peptidase alpha.
GN MEI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21293028; PubMed=11278416;
RA Shirotsani K., Tsubuki S., Iwata N., Takaki Y., Harigaya W.,
RA Maruyama K., Kiyu-Seo S., Kiyama H., Iwata H., Tomita T.,
RA Iwatsuno T., Saito T.C.;

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RT "Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
RT Rapidly and Efficiently among Thiorphan- and Phosphoramidon-sensitive
RT Endopeptidases."
RL J. Biol. Chem. 276:21895-21901(2001).
DR EMBL: AF302075; MAG18446.1; -.
DR HSSP: P08473; IDMT.
DR MEROPS: M13.008; -.
DR MGD: MGI:1351603; Me111.
DR InterPro: IPR000718; Peptidase_M13.
DR InterPro: IPR001230; Prenyl_site.
DR Pfam: PF00130; zn_mtpeptase.
DR PRINTS: PR00786; NEPRILYSIN.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN.1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN.1.
SQ SEQUENCE 742 AA; 85993 MW; 4444EAD211B2499F CRC64;

Query Match 34.9%; Score 1380; DB 11; Length 742;
Best Local Similarity 38.8%; Pred. No. 3.6e-87;
Matches 291; Conservative 148; Mismatches 267; Indels 44; Gaps 17;

QY 18 GTRIALVYFGGTVLITGLFLVSGGLSLQAKOECYCKPCCIEAAAIATSKVNLVSDPC 77
DB 19 GLAVLILLGLAVITLVG---FYSIALRDSLSKSDICTTPSCVTAARILNMDQSRNRC 75
QY 78 DNEFFACDGTWISNNPDEMPSTGYVYPMLRHNDLKTLEKTSIRRRDEALQAKI 137
DB 76 EEFYVACGWLRRHVIYLETNSRYSVFIDILRDELEVLEVLKGLDSTSQHR--PAVEKAT 133
QY 138 LYSSCNEKATIKAKAPLHLRLHSPPRMVLESNIGPEGVWSEK---KFSILDTLATF 194
DB 134 LYSSCNEKATIKAKAPLHLRLHSPPRMVLESNIGPEGVWSEK---KFSILDTLATF 194
QY 195 RGOYSNSVFIILYVSPDDKASNEHILKIDQATISLAVREDYLDNSTEAKSYDALTAKYCYPE 254
DB 187 NSQFNRRVLLDLFTMNDQNSSRHVIYIDQPTLGMPSEYFQEDNNH--VAKVLEFMT 245
QY 255 DTAVL-----LGANSRAHDKSVYRLKIAETIMIPHENTSEAMTKMSELSA 307
DB 246 SVATMLRKQDNLSEKSMVREAEVLEETHLANATVQEKRHVDYALYHMDLMEQ 305
QY 308 M--IPQDMLGYIKV---IDTRYLPHLKDISENVVAVVQYFKDLFRILIGSRKKTI 362
DB 306 RFGIKGFNMWTLFTQNLVSSVEVELF-----PDEEVVYGIPIYLEDLIDISARTM 358
QY 363 ANYLVNMYYSRIPIINSRPOYHLEFSRYIGTITLLPQWDKCVNFTESALPYVVGKMF 422
DB 359 ONYLVNMYYSRIPIINSRPOYHLEFSRYIGTITLLPQWDKCVNFTESALPYVVGKMF 422
QY 423 VDYVYFQEDKKEMMELVEGVNAFIDMLEKENEMDAGTKRKAKARAVLAKYCYPEFI 482
DB 419 IKRAFSDKSKSVRELIERISVFDNDELN--WMDESKKAQKAKANNINIEQIDYI 477
QY 483 M--NOTHVNEDLKIKSEADYEGNVLOTRTYLAQSDPEFLKRAVKTETFTPTVNAF 540
DB 478 LEDNNKHDEBEVSSLTFTYDLYFENGLOLNKNAARSILKRLREKVDOMLTIGAAYNAF 537
QY 541 YSASTNOIRFAPAGELQKPFMGTEYPRSLSYGAIYVGEHFTGHDNGRKKDKNGND 600
DB 538 YSPNRQIVFPAIGLQPPF--SKDQPSLNGIGMVIYGHITITGFDNGRNFKNKGMNL 596
QY 601 PWSSTESSEKFEKTKCMINQYSYVYKKA--GLVYKGRITGENIADNGILREAFRAYRK 659
DB 597 DMWSNFAHFFQOQOCMIYQGNFSLMADONVNFSTIGENIADNGVRAQYKAYLR 656
QY 660 WINDRQGLEBLLPGITFTNNOLFSLYAHVRCNSYRPEARQVOIGAHSPQORVNG 719
DB 657 WLAD---GKQDRLPGMLTYAQLEFINTAQYVWGSITRPEAVOSIKTVDVHSPKATYVLG 713
QY 720 AISNEEFQAKFNPSTANRKGDCRLW 749
DB 714 SIQNLPGFSEAFHCPDRGSPM--PMKRCRIW 742

```

Query Match	Best local similarity	Matches 295;	Conservative 147;	Mismatches 267;	Indels 51;	Gaps 18;
QY 18	GTITAIIVVF--VSGTVLIGTILE-----LVSQGLSLQAKQEXCLPPECIEAATAIL 67	34.8%;	Score 1375.5;	DB 11;	Length 765;	
Db 29	GAIVTIGVYRISICKQPLPLTSLHFWMDERTYVKRALRQSLKSDICTPSCVIAARIL 88	38.8%;	Pred. No. 7.7e-87;			
QY 68	SKYLVSDPCDNFREFRACDGMISNNDIPEDMPSYGYVPMLRHNVDLKLKELLEKSISRRL 127					
Db 89	ENNDQSNPCENFYQYACGGMLRHVYIPETNSRYSVFDLLIKBLEVILKGVLEDSRQHR 148					
QY 128	DTEAIDKAKTILSSCNMKEKAEKADKPLHLIRHSPFRPVSINIGPGVSESR---K 184					
Db 149	--PRAVEAKTILYSSCNMQSVIEKRDSPELLSYLK-WNGGPNVAMDK-----WNETMGK 199					
QY 185	FSLIQLATFPGQYSNSVFIRLYVSPDDKASNEHILKLDQATLSLAVREDYLDNSTEAKS 244					
Db 200	WELEROLAIVNSQFNRFRVLIIDLFTMNDQNSRHVYIIDPILGMPRSREYFQEDNNHK- 258					
QY 245	YRQALYFEMVDYAVL-----LGANSRAHDHKSYSVLRLEIKTAEIIPHEPNTS-EAM 297					
Db 259	VRAVYAEFMSVATMLRKDONLSKESAMVEEAEVLEETHLANAVPEKRDHYATL 318					
QY 298	NKNNISLISAM--IPQDWLGVIKKV---IDTRLYPHLKIDISPEYVAVVPEQFKDLFR 352					
Db 319	HRMDLMELOERFELKGNWTLFIQNVLSYSEVELF-----PDEEVVYVGIIYLEMIED 371					
QY 353	ILGSEKKTIANLYVMWYVSRIPNLSRRQYRKLEFSRYVIGQTTILLPQMDGVNFIES 412					

Dd	372	IIDSYSAPFMONITVWMLVLVDIRGSLSQRKREKRVYRKALEYTYVEVRWMRCVS	431
Oy	413	ALPYVKMPEVDYTOEDKKEEMEEIVEGVMAFPIDMLEKENEMDAGTKRKAKARAY	472
		: : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :	
Dd	432	NMESAVOSLYIKRAFSKDSKSTVELIEKTRSFVDMDELN-WMDESCKKAOEKAMNI	490
Oy	473	LAKGYEPBEFL-NDRVNEDLKAIRKSEADYGCVNLQTKRYLAOSDFWLRAAVERTEW	530
		: : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :	
Dd	491	REQOIGPDIYLEDNNKHIDEYSLSLTVEEYLFEENGLOINKNNQNSLKLRKVIDONIM	550
Oy	531	FTHPTVAAFVASTNOIRPAGELQRPFWGETPRSLSYGAIGYIVGEHTHGEDNG	590
		: : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :	
Dd	551	TIGAAYNAEFSPRNQIVPAFGILQPPFF-SKQOPSLNPGGIGMVGHEITHGFDDNG	609
Oy	591	RKYDKNGMLDWMSGTSESEERKEFKCKMINOYSITYKKA-GLNVKRKRLGENIDNG	649
		: : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :	
Dd	610	RNFDEKNGMLDWMSFNFSARHFQOOSOCMIYOYGFSEWELDNQNVNPFSTLEGINIDNG	669
Oy	650	IREAPRAVRKMINDROGLEPLLPGTFTTNOLFSTAHVCNSYRPEAPAREQVOIGA	709
		: : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :	
Dd	670	VQAATKALKRLWAD--GGKDQLPLGLMTYTAAQLFITNYAWMGSGSTRPERAVGSIXDV	726
Oy	710	HSPQFRVNGAISNSEEFOKAFNCPPNSTNMNRGDSCRW	749
		: : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :	
Dd	727	HSPKTRVIGSLQNLPGESEAFHCPGRSPMH-PMKRCRIW	765
RESULT 4			
ID	09QZV6	PRELIMINARY:	PRT: 742 AA.
AC	09QZV6		
Dt	01-MAY-2000	(TREMBLrel. 13, Created)	
Dt	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
Dt	01-JUN-2002	(TREMBLrel. 21, Last annotation update)	
DE	Soluble secreted endopeptidase delta.		
GN	MELL.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muride; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20011457; PubMed=10542292;		
RA	Ikeda K., Emoto N., Raharjo S.B., Nunthanari Y., Sakai K.,		
RA	Yokoyama M., Matsuo M.;		
RT	"Molecular identification and characterization of novel membrane-bound		
RT	metallopeptidase, the soluble secreted form of which hydrolyzes a		
RT	variety of vasoactive peptides.";		
RL	J. Biol. Chem. 274:32469-32477(1999).		
DR	EMBL: AF157106; AAF13153.1; .		
DR	HSSP: P08473; IDMT.		
DR	MEROPS: M13.008; .		
DR	MGD: MG1:1351603; Me11.1.		
DR	InterPro: IPR000718; Peptidase_M13.		
DR	InterPro: IPR001230; Prenyl_site.		
DR	InterPro: IPR001030; Zn.MPeptidse.		
DR	Pfam: PF01431; Peptidase_M13; 1.		
DR	PRINTS: PR00786; NEPRILYSIN.		
DR	PROSITE: PS00294; PRENYLATION; UNKNOWN_1.		
DR	PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.		
SQ	SEQUENCE 742 AA: 85945 MW; CFSFFPD982471157 CRC64;		
Query Match	34.7%;	Score 1373;	DB 11; Length 742;
Best Local Similarity	38.7%;	Pred. No. 1 le-86;	
Matches 290; Conservative 149;	Mismatches 267;	Indels 44;	Gaps 17;
Oy	18	GTRIALVFVFGGLVTLLTLFLVSOGILLQAKOEYCLKRECTEAANAAILSKVNSVDCP	77
		: : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :	
Dd	19	GLMWLLIILGAIYTLGV--FYSIALRDSSLKSDICTTPSCVIYAARILENNDOGRNPC	75
Oy	78	DNEFRACDGWISNNPIPEDMPSTGYVPWLRRHVNDLKLKELLEKSISRREDTAIOAKTI	137
		: : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :	
Dd	76	ENFYQYAGCGGLRHVHPETNSRSYVDLIIRDELEVILKGVLSDTSQRH--PAVERAKTI	133

DR InterPro: IPR0001230; Prenyl\_site  
 DR Pfam: PF01431; Peptidase\_M13; 1.  
 DR PRINTS: PR00786; NEPRILysin.  
 DR PROSITE: PS00294; PRENYLATIN.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 DR SEQUENCE 765 AA; 88651 MW; 567D3C17764C0F3F CRC64;

Query Match 34.6%; Score 1368.5; DB 11; Length 765;  
 Best local similarity 38.7%; Pred. No. 2,3e-86;  
 Matches 294; Conservative 148; Mismatches 267; Indels 51; Gaps 18;

OY	18	GTIALVVF--VGGTIVLTITLF-----	-LYSQGLSLQAKOEKCLKPECIEAANAII	67
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	29	GAIVTLGVFYSIGKQPLPLTSLHF	EMDEKIVYKRLRRSLKSDICTTPSCVIAANAII	88
OY	68	SKVLASVDPDGNFRFACDGMISNNDPI	EDMDSYGYPWLRHNVDLKLELLEKSISRR	127
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	89	ENMDSNRPCEENRYQAACGGLMHHYI	PETNSRYSVFDELRLDELEVIILKLEDS	148
OY	128	DTETIQAKLILYSSCAMEKAIEKADK	PLHLIRHSFPRWPLENIGPBEVNSR---K	184
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	149	--PAVEAKTLIYSCNMOSVIERDESE	PLSLK -WGGWPVALDK-----	199
OY	185	FSLIQTATLRGOYSNSVFRILYSP	DDKASNEHILIKDQATLSLAVREDYLD	244
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	200	WEIERQIALVINSQFENRRVYLIDF	IMDDQNSRHRIYIDQPLTGPSPREYFY	258
OY	245	YRDALYKFWYDQVYL-----	LGANSSRREHDSKSVLRLEKIAEIMPHEN	297
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	259	VRRAYPEFMTSVATMLRKDONLSK	SAMVREMAVLELETHLNAVYPOKREID	318
OY	298	NKNINIELSM--IPQEDMLGIYIKV--	IDTRLYLKDISPSENYYVRVPOYFNDLFR	352
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	319	HRHDLWELORRGLKGFENNTLFI	QVNLSSVELEF-----	371
OY	353	ILGSEKKTITANTLVWRMYRSRIP	MLSRFOYMLFEFSRVIGQTTLLPQMD	412
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	372	IIDSYSARTMONTLVWRVLYDRIG	LSQRFREARVDIKALITYTVEVNR	431
OY	413	ALTYVYVGMFVDVYIQEOKKEM	ELVGCVMATIDMLEKENEMDAGTRKAK	472
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	432	NMMSAVGSILYIRAVSKOSKST	YRELIRKISVVDMLDELIN -WMD	490
OY	473	LAKVYGERIM--NDTHVEDLKA	IFSEADYFENSVQOTRRYLAQSOFF	530
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	491	REQIGVPTIILEDNKKHIDEE	YSSTLTFEDILFEINGQNLKNNQSLK	550
OY	531	FINPTTYVAFYASLTNQIRF	PAGELQRFPEWTEYPRSLSYGALIV	590
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	551	IIGAAVVAVFASPNNQIVF	PAGILOPPEF -SKQOPSLINFG	609
OY	591	RYKDNKGLDPMWSTSESE	EKEFKTKCINQOYSVYWKKA -GLNV	649
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	610	RNFEDRNGMLDPMWSFSA	RHFGQOSQCMITYQIGFSEWELAD	669
OY	650	IREARVATKMINDRROGLE	EPILLPGITTTNNOLFSLSYAHVACNS	709
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	670	VQAQAKALIMLAD---GK	QDRLPGLINTLYAOLFINTAQV	726
OY	710	HSPQFRVNGAISNSE	EFQKAFNCPPTSTNNRMDSCRIM	749
		:   :   :   :   :   :   :   :	:   :   :   :   :   :   :	
Db	727	HSPLKRYVLSLQNLPG	FSFAFCRPGSPWA -PMKRCRIM	765

RESULT 6  
 O9ERR2  
 ID O9ERR2 PRELIMINARY; PRT; 779 AA.  
 AC O9ERR2  
 DT 01-MAR-2001 (TEmblrel. 16, Created)  
 DT 01-MAR-2001 (TEmblrel. 16, Last annotation update)  
 DT 01-JUN-2002 (TEmblrel. 21, Last annotation update)



GN MELL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21293028; PubMed-11278416;  
RA Shirokani K., Tsuduki S., Iwata N., Takaki Y., Harigaya W.,  
Matsuyama K., Kiyu-Seo S., Kiyama H., Iwata H., Tomita T.,  
Iwatsubo T., Saido T.C.;  
RA Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most  
Rapidly and Efficiently among Thiorphan- and Phosphoramidon-sensitive  
RT Endopeptidases.";  
RT J. Biol. Chem. 276:21895-21901(2001).  
RL EMBL: AF302077; AAC18448.1; -.  
DR HSSP: P08473; IDMT.  
DR MEROPS: M13.008; -.  
DR MG1: M1351603; M11.  
DR InterPro: IPR000718; Peptidase\_M13.  
DR InterPro: IPR001230; Prenyl\_site.  
DR InterPro: IPR00130; Zn\_M13peptidase.  
DR Pfam: PF01431; Peptidase\_M13; 1.  
DR PRINTS: PRO0786; NEPRILYSIN.  
DR PROSITE: PS00294; PRENYLATION; UNKNOWN\_1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
SQ SEQUENCE 779 AA; 89709 MW; 5E48CA530828584B CRC64;

Query Match 34.4%; Score 1361.5; DB 11; Length 779;  
Best Local Similarity 37.0%; Pred. No. 7.3e-86; Indels 81; Gaps 17;  
Matches 291; Conservative 148; Mismatches 267;

18 GTRIALVYVGGTILGLIIFLVSGILSLAQKQECYCKPCIEBAALISKNVLSVDP 77  
19 GLMVLILLGLAIVTLG---FYSLALDSSLKSDICTPCVLAARILENMQSRNPC 75  
78 DNEFRACDGMISNIPEDMDSYGVYVWLRHNDLKLKELLEISRRPTTEAIOAKI 137  
76 ENFYQACGMLRHVHIVPTNSRYSVFDLRLDELEVIKGLVEDSTOHR--PAVERAKT 133  
138 LYSSCNKAEKADKPLHLIRSPFRPYLESNIGPEGVMSR--KPSLLQTLATF 194  
134 LYSSCMOSVYERKDESEPLSLYK--WYGMVPAAMK-----WNETMGKMLEROLAVL 186  
195 RGOYSNVPFRLYVSPDKASNEHILKLDQATLSLAVERDYDINSTKASYDALYKXPV 254  
187 NSQFNRYVLDLFTWMDQSSRHVYIDQPLGMPFSREYFOEDNNH--YKATLEMT 245  
255 DPAVL-----LGANSSRAHDKSVLRLEIKIAELIMPHENKTS--EAMYNKMISEL 307  
246 SVATMLRRDONLSKESAMREMAEYVELETHLANATVQEKRHVDYALHHRMDLMELOE 305  
308 M-----IPQFDLGIKKV-----IDNR 325  
306 RFGKLDKRVSLCSPGPGTHSVDOAGLELGNPSPADSRVGLKGFNNLTFLQNLVLSVEYE 365  
336 LYPIKIDISPEENVVAVPQYKDFRLIGSEKRTIANTLVWRYVSRIPNLRRFOYR 385  
366 LF-----PDEEVVYVGIPILEMLIDISYAKRTMONLVRLVYDRIGLSLSQRFKA 418  
386 WLEFSRVIGTTLTPQMDKCNFIESALPVYVGMFVDYVFOEDKEMMEELVEGYRMA 445  
419 RVDYKALXGTTVEEVNRRECVSYVNSMESAVGSLYIKRAFSDKSTYRELEIKIRSY 478  
446 FIDMLEKENEMDAGTKKAKAKARAVLAKYGPETIR--NDTVNEDLKAIFSEADYF 503  
479 FVDNIDELN--WMDSESKKAKQAKANNIREOLIGTPIYIIEDNNKHLDEYSLSFEDLYE 537  
504 GNVLTGRKYLQSDFFMLKAKAPKTEFTNPTVNAEYASSTNOIIRPAGELQPFVWGT 563  
538 ENGLQMLKNNAOBSLKLREKVDQNLWITGAAYVNAFYSPPRNQIVPAGILOPFF--SK 596  
564 EYPRSLSYGALGYVGHETHGFDNNNGKRYDKNGNLDMWMSFESEKFEKTKCMINGYS 623

DB 597 DQPSLNFEGIGMVGITHTHGFEDNGNRPDKNGMLDMWNSFSARHFOOQSCMIYOYG 656  
OY 624 NYWYKKA--GLANYKGRRTIGENIADNGLGREAFRAYRKINDRROGLEBPLITGTFINNQ 682  
DB 657 NPSMELADNONNGFSTIGENIADNGVQAOYKAYLRMLAD--GGKORLPLGLNTLYAQ 713  
OY 683 LEFLTAHVRCNSYRPEARDEVOYGAHSPPOFRVNGAISNSEEFQKAFNCPNPMNNG 742  
DB 714 LFEINIAQWCGSGYRPEFVQSTKIDVHSPKTRVLSIQNLPGPSEAFHCPGSPMH--P 772  
OY 743 MDSCLW 749  
DB 773 MKRCRIW 779

RESULT 7  
ID 093394 PRELIMINARY; PRT; 770 AA.  
AC 093394;  
DT 01-NOV-1998 (T-EMBLrel. 08, Created)  
DT 01-NOV-1998 (T-EMBLrel. 08, last sequence update)  
DT 01-JUN-2002 (T-EMBLrel. 21, last annotation update)  
DE Neprilysin.  
GN NEPL.  
OS Perca fluviatilis (Yellow perch).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;  
OC Percidae; Perca.  
OX NCBI\_TaxId=8167;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-OVULATORY OVARY;  
RX MEDLINE-99445407; PubMed-10514552;  
RA Langenau D.M., Goetz F.W., Roberts S.B.;  
RT The upregulation of messenger ribonucleic acids during 17alpha,  
RT 20beta-dihydroxy-4-pregnene-3-one-induced ovulation in the perch  
RT ovary.";  
RL J. Mol. Endocrinol. 23:137-152(1999).  
DR EMBL: AF07612; AAC28366.1; -.  
DR HSSP: P08473; IDMT.  
DR MEROPS: M13.001; -.  
DR InterPro: IPR000718; Peptidase\_M13.  
DR InterPro: IPR001230; Prenyl\_site.  
DR InterPro: IPR00130; Zn\_M13peptidase.  
DR Pfam: PF01431; Peptidase\_M13; 1.  
DR PRINTS: PRO0786; NEPRILYSIN.  
DR PROSITE: PS00294; PRENYLATION; UNKNOWN\_1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
SQ SEQUENCE 770 AA; 88135 MW; D29F216CB041BACC CRC64;

Query Match 33.7%; Score 1335; DB 13; Length 770;  
Best Local Similarity 38.0%; Pred. No. 5e-84;  
Matches 294; Conservative 146; Mismatches 283; Indels 50; Gaps 21;

3 AETGS--SVERG--KKNRGTALVYVGGTILGLIIFLVSGILSLAQKQECYCKPCIEBAALISKNVLSVDP 77  
22 AEAQDLMRMEINPPKSKAKKPRWTSLEV---GLTFIVSLFETIVALLITLPAQKDEICT 78  
OY 56 KPECIEAAAILSKVNSVDPDNFERRFACDGMISNIPEDMDSYGVYVWLRHNDLKL 115  
DB 79 TGDCTQASRLIENMDSDVPCDNFYQACGMLKRIIIPISRSRSTPDLIDLEVL 138  
OY 116 KELLEISRRDFAIOKALILYSSCMNEKAEKADKPLHLIRSPFRVYL-----E 171  
DB 139 KGVLEK--TDEEALSLRAKATVYKSCINSELILRCGAPLIDML--PDVEWEPVADVNM 195  
OY 172 SNIGEGVWSEKESLQTLATFRGOYSNFIILYVSPDKASNEHILKLDQAT--LSLA 230  
DB 196 TNYG-----KTMVLEVYIAKLEKYGTLQVNFVGTDRDSNYIIHFDDQTNGLL 248  
OY 231 VREDYLDNSTEAKSRDALYKPMVDTAVL-----GANSRAE--HDKSVLRLEIKIAEI 264

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Db 249 SRDYACTGPAEACR-AYEKEMIDLAKLIRIDRGILNISTEDTIREKRYMDLERDIANA 307
Qy 285 MIPENRTESE-ATYKKNISLSLMT-----POFMDLGYIKKVIDTFLYPHLKDISPE 337
Db 308 TDTEDENRNPPVLLTKNKGDLNANFTLEVESQVFDMSVETAKIMTVM-----SVPTD 363
Qy 338 NVVVVPOVDFEFLRIGSERKKTIANLYVMRYVSRIRNLSRRQYRMLESRYIOGT 397
Db 364 KVIYSPNYRRLNLILARYNKDILONYVMRYVSRIRNLSRRQYRMLESRYIOGT 423
Qy 398 TLDPOMKCVNFIESALPYVGMEDVYFOEDKEMMEELVEGYMAFIDMLEKENEM 457
Db 424 SEAAVMQCALVYNNMNDVAVGLYQVAFSEKSEKLEMEIKDIREFISILD-DLTM 482
Qy 458 DAGTKRAKARAVLAKVGYPEFIMNDPHVEDLKAIFSEADYFGVLTOTRYKLAOS 517
Db 483 DAETKRAAEKARAIERIGYSDNIKDKYLNNEYNDLAYSSEFEENILNLEYOKR 542
Qy 518 FFWLRAVKTETFTNPTVNAFYASTNOIRFPAGELQKPEFWCTEYPRSLYGATGY 577
Db 543 LRKLRYKKEEMVGAAYVNAFYSSKNOIYFPAIGLQPEF-SKGAOKSLNIGIGV 601
Qy 578 VGEHTGFEDNNGRYKNGNDLPMWSTSESEKFEKTKCINIYSNYAKA-GLNVK 636
Db 602 IGHETIGHFDNGRYNDKDGDLKMTWGTSTDRFLDSKCTVNOYGNFSDLANGLHNG 661
Qy 637 KRTLGENTADNGLEAPRAYRKATYNDROGLEPPLPGITFTNNOLFYSYAHVRCNS 696
Db 662 NNTLENTADNGIQAQVAKKNY--EKHG-EEPSLPGIMLSHNOLEFIMFQVWCGTH 718
Qy 697 REAPAREVOIGAHSPPOFRVNGAISNSEFOKAFNCPSPSTANKRGDSRLM 749
Db 719 REQAVNSIKYDVHSPGKFRVYLSLQNPPEAKAFKCKNSYVPA-NICRVW 770

RESULT 8
Q96P9 PRELIMINARY; PRT; 770 AA.
AC Q96P9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Neprilysin-like metalloproteinase 2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21444797; PubMed-11560781;
RA Bonvouloir N., Lemieux N., Crine P., Boileau G., Desgroselliers L.,
RT of MME2, a gene coding for a novel human member of the neutral
RT endopeptidase-24.11 family.
RL DNA Cell Biol. 20:493-498(2001).
DR EMBL; AF336981; AAL08942.1.
DR MEROPS; M13.008;
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR001330; Prenyl_site.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 770 AA; 88523 MW; DP9C08F4A56A3B CRC64;

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Query Match 33.7%; Score 1332.5; DB 4; Length 770;  
 Best Local Similarity 39.2%; Pred. No. 7.4e-84;  
 Matches 284; Conservative 145; Mismatches 258; Indels 37; Gaps 17;

Qy 42 QGLSLQAKQVEYCKPCEIAAAAILSKVLSYDPCDNFRFRCQDGMISNPIPEDMPSY 101  
 Db 68 RGIREQVEVEVCTPCVIAAAILQNMPTTEPCDDVYQFACGGMILRRHVITPINSKY 127

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Qy 102 GYVFWLHNVDLKLLEKSISSRRDTEAIOAKILYSSCMNEKAIKAKPLHLIR 161
Db 128 SIFVRLDELEVLITKAVLENST--KDRAVEAKARILYSCNQSQVTEKRSQPLDIL- 184
Qy 162 HSPRMPVLESNIGPEWSER--KSLLOTLAEFRGYSNFTIRLYVSPDKASNEH 218
Db 185 EYVGWFWVADR-----NNEVYGLMELEEROLALMNSQFNRRVILDFINNDQNSRH 238
Qy 219 ILALDQATLSLAVREDYLDNSTEAKSRDALKEVNDRAVL--GANSR-----AEDMK 272
Db 239 IIVDPTLGMPSREYFNGSNRK-VREAYLQFVAVATLLREDANLPRSCVQEDMV 297
Qy 273 SVRLKIKTAEIMIPENNTSE-AMYNKNISLSAM--IPQFMDLGYIKKVIDTFLYPH 329
Db 298 QVLELETOAKATVQEEHHDVIALYHMGLEELQSGFGLGFWTLFIQVLS----- 352
Qy 330 LR-DISPEENVVVRPOVFKDLFRIGSERKKTIANLYVMRYVSRIRNLSRRQYRMLE 388
Db 353 VRIKILPDEEVVYGIPLQNLNENIDITYSARTIQNLVWRLVLDRLGSLQREKDRVN 412
Qy 389 FSRVIGSTTLLPOMDKVNFIESALPYVGMEDVYFOEDKEMMEELVEGYRAFTD 448
Db 413 YKALFGRVVEEVRKRECVGYVNSNMENAVGSLYREAFPGDSKSMVRELIDKRYVVB 472
Qy 449 MLEKENEMDAGTKRAKARAVLAKVGYPEFTINDTH--VVEDLKAIFSEADYFGV 506
Db 473 TLD-ELGMDEDESKKAKQEKMSIREQIGHPDYLEMNRRLDEEYSNFSEDLFEENS 531
Qy 507 LOTRYKLAOSDFWFLRAVPTETFTNPTVNAFYASTNOIRFPAGELQKPEFWCTEY 566
Db 532 LQNLKVAQBSLRKLREKVPDNLITIGAAYVNAFYSPNRQIYFPAIGLQPEF-SKEP 590
Qy 567 RSLSYGAIYVGEHTGFEDNNGRYKNGNDLPMWSTSESEKFEKTKCINIYSNY 626
Db 591 QALNFGIGVYGHETIGHFDNGRNFDPKNGMMDMWSNFSTQHPRESECMYIOGYNS 650
Qy 627 WKAG-LNVGKRTIGENTADNGLEAPRAYRKATYNDROGLEPPLPGITFTNNOLF 685
Db 651 WDLADEQNVGENTLENTADNGVQAQVAKLKW--AEGKQDQPLGDLTHQGLF 707
Qy 686 LSYAHVNCNSYREAPAREVOIGAHSPPOFRVNGAISNSEFOKAFNCPSPSTANKRGDS 745
Db 708 INYQVWCGSYREPAIQSIKTDVHSPKRYVLSLQNLAAFDTHCARCTPMH-PKER 766
Qy 746 CRM 749
Db 767 CRM 770

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RESULT 9
Q9DGN6 PRELIMINARY; PRT; 752 AA.
AC Q9DGN6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Endothelin converting enzyme-1.
GN ECE-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20363660; PubMed-10903177;
RA Takebayashi-Suzuki K., Tanigisawa M., Gourdier R.G., Kanawa N.,
RA Mikawa T.,
RT "In vivo induction of cardiac Purkinje fiber differentiation by
RT co-expression of preproendothelin-1 and endothelin converting enzyme-
RL Development 127:3523-3532(2000).

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RESULT 10	
Q28868	
ID Q28868	PRELIMINARY; PRN: 758 AA.
AC Q28868;	
DT 01-NOV-1996 (TREMBLER. 01, Created)	
DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)	

Query Match	31.7%;	Score 1253.5;	DB 6;	Length 758;
Best Local Similarity	38.0%;	Prod. No. 2.2e-78;		
Matches 283;	Conservative 121;	Mismatches 280;	Indels 61;	Gaps 21;

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01 23 LVFVGGTIVLTITLFLYSGSLLSLAKOBYCKLCEPCIEIAAAILSKVNSLVSJCDNFR 02
02 57 LVVYV-ALLAALVACLAVLIDIOYTQTPBVCSEACISVTSISLSDMPVDFCDOFFL 115
03 83 FACDGMISNPNIPEDMPSYGYWMLRHNVDLKLELLESISRDRDPAIOKAIILYSSC 142
04 116 YAGGMWKNANPVADGDSRGGTFSNIMWNOAIIKHLLENSTA--SVSEAKRAYYIRAC 173
05 143 MNEKAITEKDAKXLLHLHSHSPFRMPVLESNIGEGVWSEKRSKLQTLATFRCQYSNV 202
06 174 MNEIRTELKAKMLIELKGL-GNNI-----TGWMDNQFO--DILQAVVTSYHTNSP 223
07 203 FIRLYSPDDKASNEHILKDOATISLAVREDYLDNSTEKSRYDLAKFYNDVAVILGA 262
08 224 FFYSYVADSKNSNVNOIVDQSGIGLFSRYYL-NKTEWKKVLYGILMYNOVLGKLLG 282
09 263 NS-SRAEHDKMSVLEIKLAEIMIPHENRTSEAM-YKNKNISELSAMIPQDMLYIKK 320
10 283 GAEDTIRPOMQOIIDETALANTTIPQERBREELIYHKYTAELQTLAPAINMLP--- 339
11 321 VYDTRLYEHLKDISPENNVYVPQYFDFLPIIGSEKKTIANYVWYKYSRIPNLSR 380
12 340 -LNTIFY--VEINSEPIYIDRELSKYSTLLSIDKCLINMYMNLVYRTSEFLDQ 396
13 381 RQYVWMLSESVIGT--TLLPQMDCVNFISALPYVVGKMPVDYTFQDKKEMMEELY 439
14 397 RQDDADEFMWYGTCKTKLCPMKCVSDTENTGFMALGPMFKATFADSKNSIASETI 456
15 440 EGYRAFIIDLMEKENEMDAGTKRKAKERARAVLAKVYPERFI-----NDPHVNE 490
16 457 LEIKKAFESTL-STLKWMDDETRKSAEKADALYNNIGVPIFINDPRELDKRVNDTAVP 515
17 491 DLKAIFFSADYEGVWLOTIRKYLAOSDFW-----LKRKAVKTEWFTNPTTYNAISAS 544
18 516 DL-----YFENAMF-----PFSKRVYADOLKRAPRMDQMSVTPPNNVAYSIP 560
19 545 TNOIRPAGELOKPFECWETEPRLSLGALGVYGHGEPHGFDDNNGKRYDNLNGMLPWWMS 604
20 561 KNEIYFAGIOLAPYITSS--PNMLNNGGIGVYVGHGELHHAIDDGGRXDGLRPMWK 619
21 605 TESSEKFEKTKCOMINQOSNYWYKAGLANYKGRKTLGENTADNGLREAFRAYYIKKINDR 664
22 620 NSSYEAFAKQTLACWQGNV--SVNGEPVAGRTIGENTADNGGIGKATRAYYQWV--K 675
23 665 RQGLEEPLGITEFTNNQLEFSLAHVQNSYREPEARREVOVGASHPQFVNGAISNS 724

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Db 173 APPSPDELPVYTKAKNLKYSCLDETNDARGIDYKQMLSSSTIGEWPLISS-----AFN 226  
 Qy 182 ERKESLQTLAFPGQYNSVFIIRLYSPDOKASNEHLIKLDOATLSLAVEDL--DNS 239  
 Db 227 ESEFPITAIK-R-ANIGPGVVAFYGTGDKNSKILKLDQAFGLPGQRYRVRPND 285  
 Qy 240 TEANSYRDALYKFWNDPAVLGG-ANSSRAEHDKSVLRLKIAEIMI-PHENETSEAMY 297  
 Db 286 TYKAEYETLYR-----VAELGFPADPAEKDADVDFEQMIOISVRAIRRNANAVF 341  
 Qy 298 NKMNSELSE--MIPQFWLGIYKVIDRLYPLHK-DISSENVYVVRVPOYFQDLERIL 354  
 Db 342 NPMTLAIDODESSPELNFSLITTVMSA---PEVAVSGDELTIMNSPEYFNRLDIL 398  
 Qy 395 GSEKRTIANTLVNRMVYSRIPINLSRREQYKWLSESRVIOGTTLTPQMDKCVNFISAL 414  
 Db 399 RNTPKRTIANTYIMRTITISYGLTQYFKDREFETKATYIEIVOPRELCTISFVRNV 458  
 Qy 415 PYVVGKMFVDYVFOEDKKEMLEVEGRVAFIDMLEKENEMDAGTKRKAKARAVLA 474  
 Db 459 GFILSKPVDKFEFSEADVALEMISGLQSAFNEIYD-EVEMDDETKVYAREKNDALYS 517  
 Qy 475 KVGYPEFIMNDTHVEDLKAIFSEADYFGVNLQTKYLAOSDFFWLKAAPKTEWFTNP 534  
 Db 518 KIGYPEFVINSTRLTELENTYNTYNDYFENILSKNKVNVDSFERSLRELYDKQWERSP 577  
 Qy 535 TTVNAFYASTNQIRFPAGELQKPFEMGTXPRLSYGAIGVYIGHEFTGDFDNGGRYD 594  
 Db 578 PTVNAVYKAGNEIYFPGILQSPVF-HVDPKTLNGSISIVITGHETHDFDQKRLYD 636  
 Qy 555 KNGNIDPMWSTSESEKEKTKCMINOYSNYWKAGLNVKGRKPTLGENIADNG----- 648  
 Db 637 KNGNIDPMWSTSESEKEKTKCMINOYSNYWKAGLNVKGRKPTLGENIADNGSVKSL 696  
 Qy 649 GLREAFRAYRWINDROGLEPILPGITTEFNNOLEFISYAHVRCNSYRPAAREQYQIG 708  
 Db 697 GRTKLGOSTRK-----EAPLLPGLOXTNDOLFETISQTCNMRTDALISSIRSG 747  
 Qy 709 AHSPPQFRVNGAISNSEEFQAFNCPPNSTNNRGDSCRLW 749  
 Db 748 VHSPPQFRVNGAISNSEEFQAFNCPPNSTNNRGDSCRLW 787  
 RESULT 13  
 Q9BLH1 PRELIMINARY: PRT; 772 AA.  
 ID Q9BLH1  
 AC Q9BLH1:  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Neutral endopeptidase 24.11.  
 GN BMEP-L.  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Bombycoidea; Bombycidae; Bombyx.  
 OC NCBL\_taxid=7091;  
 OX NCBL\_taxid=7091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kawasaki H., Zhao X.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Zhao X., Mita K., Shimada T., Okano K., Quan G., Kanke E.;  
 RT "Isolation of a 20-hydroxycycloindole nepilysin (neutral  
 RT endopeptidase 24.11)-like gene and its expression in wing discs during  
 RT metamorphosis of Bombyx mori."  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB048208; BAB33300.1; -.  
 DR HSSP; P08473; IDMT.  
 DR InterPro; IPR000718; Peptidase\_M13.  
 DR InterPro; IPR001230; Ptenyl\_site.  
 DR InterPro; IPR000130; Zn\_MTPeptide.

DR Pfam; PF01431; Peptidase\_M13; 1.  
 DR PRINTS; PRO0786; NEPILYSIN.  
 DR PROSITE; PS00294; NEPIRYLATIN; UNKNOWN 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
 DR SEQUENCE 772 AA; 87763 MW; B0D3330EAF4F0D56 CRC64;  
 Query Match 30.8%; Score 1219; Db 5; Length 772;  
 Best Local Similarity 37.6%; Pred. No. 5; Se-76;  
 Matches 264; Conservative 137; Mismatches 276; Indels 26; Gaps 16;  
 Qy 52 EYCLKPECIAAAAIISKVNLSDPCDNFRFACDGMISNPIPEDEMGYIPYIRNAV 111  
 Db 91 EYCSAGCIIHTAARLLINDEKVDPCDNFDFACGSLNTRIRIPDKTSVNFSSITDOL 150  
 Qy 112 DLKIKELLESISRDRDTEALQKATILYSSCMERKAEKADKPLHLIRHSPFVPE 171  
 Db 151 QEOIRSLDEPVT-PEPPRFVIAKTLQYQCMKRTAIEARGVPLDMLKRLG-GMPVLD 208  
 Qy 172 SNIGPEGVMSERFSLQTLATER-GQYSNVFIIRLYSPDOKASNEHLIKLDOATLSIA 230  
 Db 209 GQ-----SMDENFSEMGQSYKFRDAGSYVDYELDSISVDVKNSTRVYIDLOQASIGIS 263  
 Qy 231 VREDYLDNSTEAKSYRDALYKFWNDPAVLIGANSSRAEHDKSVLLEIKIAEIMPE- 289  
 Db 264 --REYINRGFSDLVQ-AYEYVVDIALIGADKRTATELKSLOFEKMLANISLPLEK 320  
 Qy 290 NRTSEAMYNKMNSELSEAMIPQFDWGIYKVIDRLYPLKDISSENVYVVRVPOYFKD 349  
 Db 321 RNNATSLYNMTIAELQOKPKYPLLEYIRL---LAPHI-IVDVNELTISVPEYITD 375  
 Qy 350 LFRILGSEKRTIANTLVNRMVYSRIPINLSRREQYKWLSESRVIOGTTLTPQMDKCVNF 409  
 Db 376 LEALIEKTPRQVQANYVMHVRVAGASYLDDLRQLAVITLALSGKTERESRMEKCAJD 435  
 Qy 410 IESALPYVVKMFMVDYVFOEDKKEMLEVEGRVAFIDMLEKENEMDAGTKRKAKERA 469  
 Db 436 TSMSMSTAVGALYIRKYFNENSRANLAEVNDIRQOFRKTLIV-DWMDMTRQOELENA 494  
 Qy 470 RAVLAKYGEFIMNDTHVEDLKAIFSEADYFGVNLQTKYLAOSDFFWLKAAPKTE 529  
 Db 495 DAAASHAYISEMLDNNRLLEFYSGLEMSEHLMESVLNLTETTYLRLGKLAPEPNKTD 554  
 Qy 530 WFTN--PTVNAVYKAGNEIYFPGILQSPVF-HVDPKTLNGSISIVITGHETHDFDQKRLYD 587  
 Db 555 WYTHGRPAIYNAFYSSIEHSIQPAGILQSAF-SAKRPAYMNGAIGVYIGHEITHGFD 613  
 Qy 588 NNGKRYKNGNIDPMWSTSESEKEKTKCMINOYSNYWKAGLNVKGRKPTLGENIADN 647  
 Db 614 DQGRQFDKCNLVDWQWQEMTKERYLDKACIIDQYSNYTKYEGVLKNGVNTGENIADN 673  
 Qy 648 GLREAFRAYRWINDROGLEPILPGI-TYNNOLFEISYAHVRCNSYRPAAREQYQ 706  
 Db 674 GGIKKATYAYQANTH--RHS-EEARLPGLEKYEPRQLFWLSAANTWCAYIRNAILRLIT 730  
 Qy 707 IGASPPQFRVNGAISNSEEFQAFNCPPNSTNNRGDSCRLW 749  
 Db 731 TGFHAPGRFRVIGPMSNMEEFASDFKCPMGSPMNP-D-KCKKW 772  
 RESULT 14  
 O16796 PRELIMINARY: PRT; 848 AA.  
 ID O16796  
 AC O16796:  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 97.1 kDa protein.  
 GN F18A12.8.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBL\_taxid=6239;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "genome sequence of the nematode C. elegans: a platform for  
 investigating biology. the C. elegans Sequencing Consortium.",  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R., Ozersky P., Le T.T.;  
 RT "The sequence of C. elegans cosmid F18A12.",  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RT "Direct Submission";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF016688; AAB66079.2; -;  
 DR HSSP; P08473; IDMT.  
 DR InterPro; IPR000718; Peptidase\_M13.  
 DR InterPro; IPR001230; Prenyl\_site.  
 DR InterPro; IPR000130; Zn\_MTPeptide.  
 DR Pfam; PF01431; Peptidase\_M13; 1.  
 DR PRINTS; PR00786; NEPRILYSIN.  
 DR PROSITE; PS00294; PRENYLATION; UNKNOWN\_1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 848 AA; 97061 MW; 4548FEFE5A915DA4 CRC64;

Query Match 30.5%; Score 1209; DB 5; Length 848;  
 Best Local Similarity 35.4%; Pred. No. 3.1e-75;  
 Matches 254; Conservative 140; Mismatches 277; Indels 46; Gaps 15;

QY 52 EYCLAPPCIAAAALISKVLSDPCDNFRACDGMISNNRPEDMPSGYVPMRLAHNV 111  
 DB 159 EVSTPCVCAATHTFLAAMTSDPCDDFEACGQMNQDHPIDDMYGTFAYAREQV 218  
 QY 112 DLKIKLEKSIARRDTEAIQAKILYSSCMNEKAIKADAKPLHLIHSFRRPVLE 171  
 DB 219 RQGLRVLEGEV--TESESINMARATYRSCMKTKQDELMTGPLETLELG-EMPLIQ 275  
 QY 172 SNIGPEGWSEKFSLLQTLATRGQYSNSVFIRLYVSPDKASNEHLIKLQDQATLSA- 230  
 DB 276 EN-----MDKTFENFTSLVNSRROYGVDFOLYIYDSKNTSHTLFIDQSTLALGR 329  
 QY 231 VREDYLDNSTEAKSYNDALTKEMVDVAVLL--GANSRAEH-----PMKSTLRLEKIAEI 284  
 DB 330 GTNDYIANTLTFSSHTATYRKYLQJIAHLKTDGNTLRSESENNADIEKIIDEIELAKI 389  
 QY 285 MIPH-ENRTSEAMYNNKNISELAMIPQEDWLGVIKKVIDTRLYPHLKDISPSE----- 337  
 DB 390 IYADEDERNNTRLYNKRQIIDLNLPOVDWV-----PFGQSLAPSDLHLHLP 437  
 QY 338 ----NNVVRVQYKDKLFRILIGSERKKTIANLYVMRWYSLIPNLRSRFOYRLSESRVIO 394  
 DB 438 NETEIIICELEYLQHVSELTEKTDVGLITNYVLMRVVQSVVRIIDRFEDIKODEFLKVM 497  
 QY 395 GTTTLPOMDKCVNFIETSLPYVVGKMFVDVYFOEDKKEMMELVGVNRAFDIMLEKEN 454  
 DB 498 GQOOSPPRMKDCQAVSTVPLAAGAIYVOAHQESDKHEALRMILHNRNPSADLV-RON 556  
 QY 455 ENMDAGTKRKAKKARAVLAKVGYPEFIMNDTHVNEDLKAIKSEADYEGNVLQTRKYLA 514  
 DB 557 DWDDEEKAVAIKAMSMINNIIGYPPVTDNLPRLDKQYIGLISDSDDTYIYIMKSVVMA 616  
 QY 515 QS-DEFWLKAAYKTEWFTNPVTYNAFYASSTQIIRPAGELQKPPFWGTETPRCLSYCA 573  
 DB 617 QSRFEKFLKRPDKHEFDISPAVNAFYSPKNAITFPAGIILQPPFSGT-FPKAVNYGA 675  
 QY 574 IGVIVHEHFGFDNNGRKDKGNLDPMWSTSEKFEKTRCMNOGSNYYWKAGLN 633

DB 676 IGAVIGHEITHGFDGSOYDKDGNLHMWSESSINSSEDTERRRCIVEGYGVTPKTNFR 735  
 QY 634 VVKRFTIGENTDNGDLNREAPRAYRKWINDRQGLEELLGT-TETNNOLFPLSYAHR 692  
 DB 736 VVKRLTQGENLADNGVGEAFAYOKYVENG--EEPRLEQLQOYTNQOIFVSYAHFW 792  
 QY 693 CNSYRPEARQVOYIGANSPPOFRVNGCAISNEEFQAKFNCPPNSTNRGDSCLW 749  
 DB 793 CGKKEAAMQVLTDEHSPEYFRVIGVLSNMQAFADYVKKCPRNAPVMD-HKCIW 848

RESULT 15  
 Q923T6 PRELIMINARY; PRT; 763 AA.

ID Q923T6  
 AC Q923T6  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Endothelin converting enzyme-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/  
 RA Pan H., Mahavira N., Devi L.A.;  
 RT "Mouse Endothelin Converting Enzyme-2 cDNA."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF396699; AAK83919.1; -;  
 DR MEROPS; M13.003; -;  
 DR InterPro; IPR000718; Peptidase\_M13.  
 DR InterPro; IPR000221; Protamine\_P1.  
 DR InterPro; IPR000130; Zn\_MTPeptide.  
 DR Pfam; PF01431; Peptidase\_M13; 1.  
 DR PROSITE; PS00048; PROTAMINE\_P1; UNKNOWN\_1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 SQ SEQUENCE 763 AA; 86205 MW; 4B5180BEF9BE549 CRC64;

Query Match 30.5%; Score 1208; DB 11; Length 763;  
 Best Local Similarity 35.4%; Pred. No. 3.1e-75;  
 Matches 267; Conservative 134; Mismatches 312; Indels 42; Gaps 16;

QY 4 ETGSSVETGKRRANRGTIALV---VFVGGPLVLTGTLIFVSGSLSLQAKQEYCLAPREC 59  
 DB 42 EVGFQKRRQLFGSHQTOELVLAGLIVLALLCVLAAL---WVNRDPAHSVCVTEAC 97  
 QY 60 IFAAAILISKVLSDPCDNFRACDGMISNNRPEDMPSGYVPMRLAHNVDLKLEL 119  
 DB 98 IRVAKGILIESLDRGVSPQDDEFYQSCGGMIRRNPLPNGRSRWNTFNSLMDONAILKHL 157  
 QY 120 EKSIARRDTEAIQAKILYSSCMNEKAIKADAKPLHLIHSFRRPVLESNIGP--- 176  
 DB 158 ENF-TFNSSSEKERTFTFYLSCLQSEKIEKGLKAPRLDL-----DKIGMNI 205  
 QY 177 EGVWSEKFSLLQTLATRGQYSNSVFIRLYVSPDKASNEHLIKLQDQATLSAVRDYL 236  
 DB 206 TGPMDDESF--NDVLKAVAGATYRAIPFTYVVSADSKSSNENIIOVQSGFLPSRDYL 263  
 QY 237 DNSTAKYRQALYKFMVDVAVILGANSRAEHDKSVLRLEKIAELMIPH-ENRTSEA 295  
 DB 264 -NRTANEVLTAVIYDVMELVGLVGGOPTSTREMOQVLELQILANITYVPODRREEK 322  
 QY 296 MYNNKNISELAMIPQEDWLGVIKKVIDTRLYPHLKDISPENVVVRVPOYFKDLFRILG 355  
 DB 323 IYHKMSISELQALAPAVDMLEFLSLSP-----LEIGDSEPVVYVGTETLQOVSLEIN 376  
 QY 326 SERKKTIANLYVMRWYSLIPNLRSRFOYRLSESRVIOGT-TTLPOMDKCVNFIETSL 414  
 DB 377 RTEPSILNNYILWNLVQKTSLSLDQRETAQEKILETLTYGKCKSPRMQTCISNTDAL 436  
 QY 415 PYVVGKMFVDVYFOEDKKEMMELVGVNRAFDIMLEKENMDAGTKRKAKKARAVLA 474

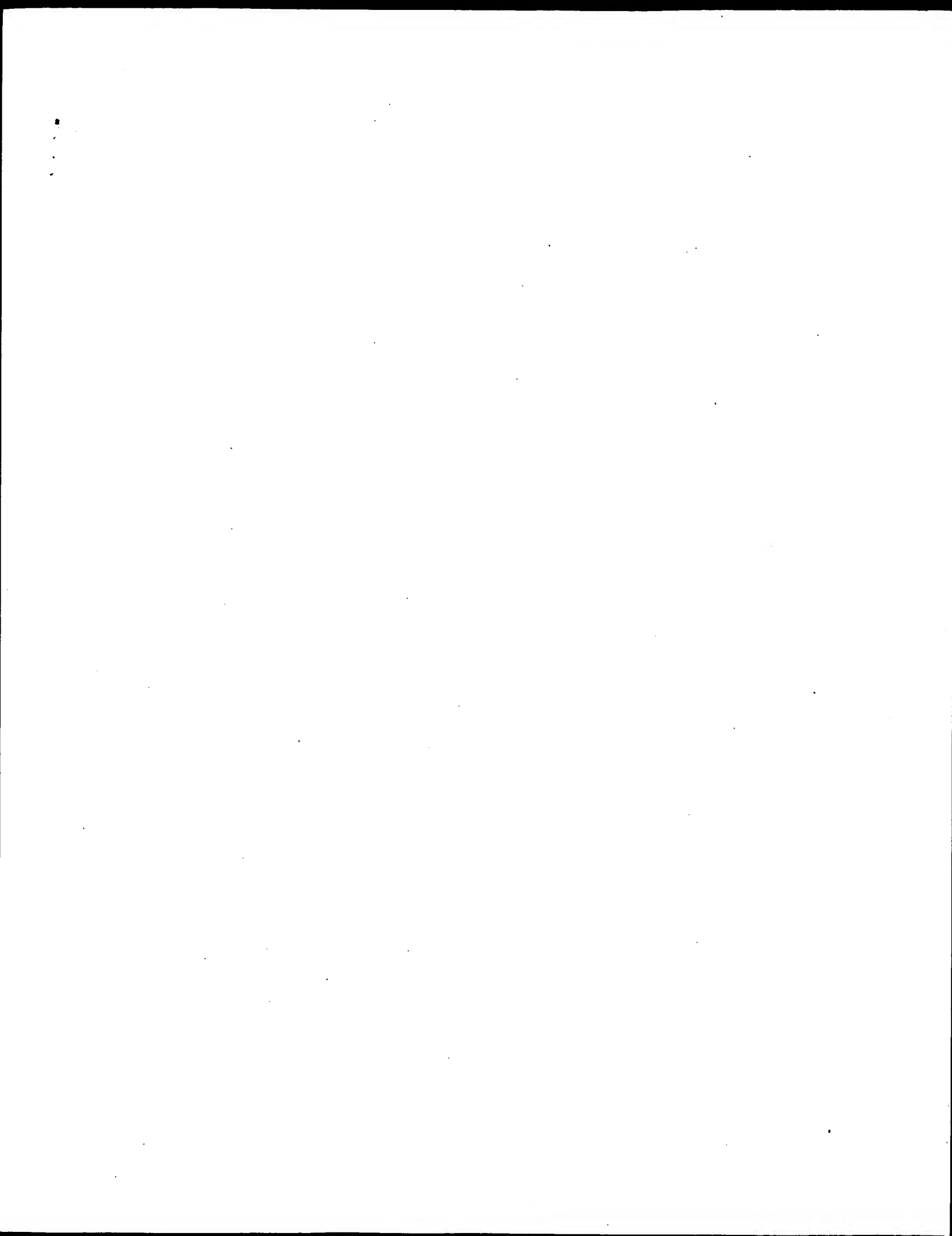


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Db 437 GFALGSLFVKATFDROSKETIAEGMINEIRSAFEETL-GDLVWMDKTRFLAKERADA1YD 495
OY 475 KVGYPEFTMNDTHVNEDEKAIKFESEADYFGVNLQTRKYLASDFFWLKRAVPTKTEWETNP 534
Db 496 MIGEPDEFLEPRELDDVDYDGYEVSEDSFQNMMLYNFSAKVMADQLKPPSRDQWSMTP 555
OY 535 TTVNAFYSASTNOLRFPAGELQKPEFMTGEXPRSLSYGAIGVIGHEFTHGFDNNGRKYD 594
Db 556 QTVNAIYLPKNEIYFPAGIILQAPFH-AHNHPKALNFGIGVYMGHELTAFDDOGRKYD 614
OY 595 KNGNLDPMWSTSESEKEKTKCMINQYSNYWKKAGLNVKGRKTLGENTLADNGGLREAF 654
Db 615 KEGNLRPMWQNESLTAFOHNTACMEQYQY--QVNGERLNGLOTLGENTLADNGGLKAY 672
OY 655 RAYRKWINDRROGLEEPLPGITFTNNQLEFLSYAHVRCNSYRPPAAREVOIGAHSPPO 714
Db 673 NAYKAWL--RKHGEQF-LPAVGLTNHQLFVGFQVWCVSVRTPESSHEGLVTDPHSPAR 729
OY 715 FRVNGAISNSEEFOKAFNCPPNSTWNRGMDSCRLW 749
Db 730 FRVLGTLNSRDFLRHFGCPVGSPPMNPB-QLCEYW 763

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Search completed: May 21, 2003, 18:49:07  
 Job time : 46 secs



Thu May 22 07:48:40 2003

us-09-913-955a-1.rag

Page 1

GenCore version 5.1.4-PS.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 21, 2003, 18:39:14 ; Search time 79 Seconds  
(without alignments)  
1263.351 Million cell updates/sec

Title: US-09-913-955a-1

Perfect score: 3958  
Sequence: 1 MEAEFGSSVEYCKKANKRTR.....AFNCPNSTNMGDSCLRW 749

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
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6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3958	100.0	749	21	Human PHX. Homo
2	3952	99.8	749	21	Amino acid sequenc
3	3928	99.2	749	21	Amino acid sequenc
4	1375.5	34.8	765	21	A murine neutral e
5	1362	34.4	753	22	Human neprilysin-1
6	1352	34.2	753	22	Amino acid sequenc
7	1351	34.1	774	20	Rat membrane metal
8	1343.5	33.9	779	22	Human neprilysin-1
9	1333.5	33.7	779	22	Amino acid sequenc
10	1332.5	33.7	770	21	A human neutral en

11	1332.5	33.7	779	23	ABR79521
12	1332.5	33.7	779	23	AAE17779
13	1332.5	33.7	779	23	AAE17779
14	1326.5	33.5	702	22	AAE17779
15	1322.5	33.4	742	23	AAE19176
16	1321	33.3	746	23	AAE17781
17	1317	33.1	743	23	AAU72903
18	1310.5	32.4	743	22	AAE07916
19	1283.5	32.4	743	22	AAE07952
20	1283.5	32.4	743	22	AAE07952
21	1283.5	32.4	743	22	AAE07952
22	1283.5	32.4	743	22	AAE07952
23	1283.5	32.4	743	22	AAE07952
24	1275.5	32.2	748	15	AAE52706
25	1270.5	32.1	750	10	AAE90393
26	1270	32.1	762	22	AAE60563
27	1265.5	32.0	750	9	AAE82940
28	1263.5	31.9	750	15	AAE52707
29	1263.5	31.9	750	15	AAE52707
30	1257	31.8	753	16	AAE76237
31	1257	31.8	753	16	AAE76237
32	1257	31.8	753	16	AAE76237
33	1257	31.8	753	16	AAE76237
34	1257	31.8	758	17	AAE03682
35	1257	31.8	758	17	AAE03682
36	1256	31.7	753	23	ABE65799
37	1248.5	31.5	758	19	AAW38369
38	1241.5	31.4	708	16	AAE76236
39	1241.5	31.4	754	16	AAE76236
40	1223	30.9	736	20	AAE41774
41	1223	30.9	736	21	AAE41774
42	1223	30.9	736	21	AAE41774
43	1221	30.8	883	22	AAE7845
44	1212	30.6	766	23	AAU82722
45	1205.5	30.5	661	22	ABE61898

#### ALIGNMENTS

RESULT 1	
AA96190	AA96190 standard: protein; 749 AA.
AC	AA96190:
XX	
DT	19-DEC-2000 (first entry)
XX	
DE	Human PHX.
XX	
KW	PHX, human; metalloproteinase; x chromosome;
KW	x-linked hypophosphatemia; hyperparathyroidism;
KW	renal osteodystrophy; phosphaturia; therapy; diagnosis.
XX	
OS	Homo sapiens.
XX	
EH	Key
FT	Peptide
FT	
XX	
FN	WC2000050580-A2.
XX	
PD	31-AUG-2000.
XX	
PF	24-FEB-2000; 2000WO-CA00201.
XX	
PR	24-FEB-1999; 99CA-2262056.
XX	
PA	(UYMO-) UNIT MONTREAL.
XX	
PI	Crine P, Bouleau G;
XX	
DR	WPI: 2000-565455/52.

Location/Qualifiers  
21.40  
/label= Transmembrane\_domain

Novel soluble human PHEX enzyme useful for treating phosphaturia and/or hypophosphatemia, is a gene product of phosphate-regulating gene having homology to endopeptidase on X chromosome

Disclosure: Fig 2; 64pp; English.

The present sequence is that of human PHEX (a gene product of phosphate-regulating gene with homology to endopeptidase on X chromosome). Absence of a functioning PHEX gene is associated with hypophosphatemia. PHEX is a type II integral membrane glycoprotein. To produce a soluble form of PHEX, the transmembrane anchor domain was modified with a signal peptidase coding sequence (see AAY96188 and AAY96189). The soluble PHEX thus comprised the active ectodomain. An inactive PHEX can also be constructed by replacement of the Glu-382 residue by a hydrophobic amino acid residue, especially valine. Soluble and inactive mutant forms of PHEX can be used to screen ligands to PHEX. These ligands are used as substrates or inhibitors of PHEX. Since PHEX is phosphaturic, an inhibitor can be used to treat phosphaturia and/or hypophosphatemia. A substrate for PHEX, or PHEX itself, can be used to treat hypophosphatemia, including its most frequent manifestations, secondary hyperparathyroidism and renal osteodystrophy.

Sequence 749 AA:

Query Match 100.0%; Score 3958; DB 21; Length 749;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MEAEFGSSVETGKKNRGTALVVEVGTGLTFLVSGGLSLQAKQECLEKCEI 60  
1 MEAEFGSSVETGKKNRGTALVVEVGTGLTFLVSGGLSLQAKQECLEKCEI 60  
61 EAAAIILSVNLSVPCNPFACDGIWNNIPEDMPSYGVYVWLRHNDLKLKELLE 120  
61 EAAAIILSVNLSVPCNPFACDGIWNNIPEDMPSYGVYVWLRHNDLKLKELLE 120  
121 KSISSRDTLEAIQAKILYSSCMNEKAIKADAKPLHLIRHSFRRPVLESNGEGVW 180  
121 KSISSRDTLEAIQAKILYSSCMNEKAIKADAKPLHLIRHSFRRPVLESNGEGVW 180  
181 SERKSLQTLATFRGOVSNVFTRLVSPDDKASNHILKLDQNTSLAVREDYDINST 240  
181 SERKSLQTLATFRGOVSNVFTRLVSPDDKASNHILKLDQNTSLAVREDYDINST 240  
241 EAKSTRDALYKFNVDIALLGANSRAEHDMKSVLRLEIKIAETMLPHENRTSEAYNNK 300  
241 EAKSTRDALYKFNVDIALLGANSRAEHDMKSVLRLEIKIAETMLPHENRTSEAYNNK 300  
301 NISLSAMITQFQDLGIRKVIDTIRLYPHLKDIPSENVVVRVPOYKDLFRILSERKK 360  
301 NISLSAMITQFQDLGIRKVIDTIRLYPHLKDIPSENVVVRVPOYKDLFRILSERKK 360  
361 TIANYLWRRVYSRIPNLSSRFQYRWLEFSRVIGQTTLLPQMDKCVNTESSALPYVVG 420  
361 TIANYLWRRVYSRIPNLSSRFQYRWLEFSRVIGQTTLLPQMDKCVNTESSALPYVVG 420  
421 MFVDYVFEQDKKMEELVEGVKMAFIDMLEKENEMDAGTRKRAKARAVLAKVGE 480  
421 MFVDYVFEQDKKMEELVEGVKMAFIDMLEKENEMDAGTRKRAKARAVLAKVGE 480  
481 FIMNDTHVNEDLKAIKFSADYFGNVLOTIRKLAOSDFEFLRKAVPKIEWNTPTYNAF 540  
481 FIMNDTHVNEDLKAIKFSADYFGNVLOTIRKLAOSDFEFLRKAVPKIEWNTPTYNAF 540  
541 YSASTNQLFEPAGELQKPFMGTEYPRSLSYGALGVIGHFTGFGDNNGKRYKNGND 600  
541 YSASTNQLFEPAGELQKPFMGTEYPRSLSYGALGVIGHFTGFGDNNGKRYKNGND 600  
601 PMWSTSESEKFEKTKCMINOSNYWKAGLANKGRTIGENTADNGGLREAFRAYRK 660  
601 PMWSTSESEKFEKTKCMINOSNYWKAGLANKGRTIGENTADNGGLREAFRAYRK 660

QY 661 INDRQGLLEPFLGTFITNNQLEFLSYAHVRCNSYRPEARQVQIGASPPQVWNGA 720  
DB 661 INDRQGLLEPFLGTFITNNQLEFLSYAHVRCNSYRPEARQVQIGASPPQVWNGA 720  
QY 721 ISNSEFQKAFNCPNSTMNRGMDSCRW 749  
DB 721 ISNSEFQKAFNCPNSTMNRGMDSCRW 749

# RESULT 2

AAY84627 standard; Protein: 749 AA.

25-JUL-2000 (first entry)

Amino acid sequence of a human PEX protein.

Human; PEX gene; Xp22.1; X-linked hypophosphatemic rickets; osteoblast; parathyroid hormone; PTH; osteoclast; bone; bone breakdown; parathyroid hormone related peptide; PTHrP; metabolic bone disease; osteomalacia; osteoporosis; osteopetrosis; Paget's disease.

Homo sapiens.

Key Location/Qualifiers

Modified-site 71 /note= "potential N-glycosylation site"  
Modified-site 238 /note= "potential N-glycosylation site"  
Modified-site 263 /note= "potential N-glycosylation site"  
Modified-site 290 /note= "potential N-glycosylation site"  
Modified-site 301 /note= "potential N-glycosylation site"  
Modified-site 377 /note= "potential N-glycosylation site"  
Modified-site 484 /note= "potential N-glycosylation site"  
Modified-site 726 /note= "potential N-glycosylation site"  
Modified-site 736 /note= "putative prenylation site"  
Modified-site /note= "potential N-glycosylation site"

W0200018954-A2.

06-APR-2000.

27-SEP-1999; 99WO-CA00895.

28-SEP-1998; 98CA-2245903.

(UWMC-) UNTV MCGIIL.

Karaplis AC, Goltzman D, Lipman ML, Henderson JE;

WPI; 2000-293177/25.

N-PSDB; AAA12670.

Diagnosis and treatment of metabolic bone diseases e.g. osteomalacia and osteoporosis comprises determining the level of parathyroid hormone related peptide in a patient -

Disclosure: Fig 2A; 52pp; English.

The present sequence is encoded by the human PEX gene. The PEX gene spans the deleted region Xp22.1 in X-linked hypophosphatemic rickets. The gene is mutated in non-deletion patients with the disorder. PEX is a cell membrane-associated protein with its active site in the extracellular compartment. The cells with the highest level of PEX expression are the



```

Db 241 EAKSTFDLAKFMDTAVLLGANSRRHDKSVLRLEIKAEIMPEHKESTENYNNKA 300
Oy 301 NISELSAMIPOFDMIGYIKKVIDIRLPHKDISPENNVYVVPQFKDLFRLLSERKK 360
Db 301 NISELSAMIPOFDMIGYIKKVIDIRLPHKDISPENNVYVVPQFKDLFRLLSERKK 360
Oy 361 TIANTLVWRMYSTRIPMLSRFRYRMLEFSRVIGTITLLPQMDKCVNFESALPYVVK 420
Db 361 TIANTLVWRMYSTRIPMLSRFRYRMLEFSRVIGTITLLPQMDKCVNFESALPYVVK 420
Oy 421 MFVYVFOEDKKEEMELVGVRRAPFDMLEKENEMWAGTKRKAARAVLAKVYPE 480
Db 421 MFVYVFOEDKKEEMELVGVRRAPFDMLEKENEMWAGTKRKAARAVLAKVYPE 480
Oy 481 FIMNDTVNEDLKAIFSEADYVGNVLOTRKYLAQSDPFWLRKAVYKTEMTNPITYVAF 540
Db 481 FIMNDTVNEDLKAIFSEADYVGNVLOTRKYLAQSDPFWLRKAVYKTEMTNPITYVAF 540
Oy 541 YSASTNOIRPAGELOKPFMGTEYPRSLSYGALGYVGHETFGPDNNGRKYDNGLD 600
Db 541 YSASTNOIRPAGELOKPFMGTEYPRSLSYGALGYVGHETFGPDNNGRKYDNGLD 600
Oy 601 PMWSTSESEKFKETKCMINQYSNTYWKAGLVNKGKRTIGENINADNGLEAPRAYRK 660
Db 601 PMWSTSESEKFKETKCMINQYSNTYWKAGLVNKGKRTIGENINADNGLEAPRAYRK 660
Oy 661 INDRQGLEPPLPGITTFNNOLFSLAHVACNSYRDEARBOVOIGASHPPQRYNGA 720
Db 661 INDRQGLEPPLPGITTFNNOLFSLAHVACNSYRDEARBOVOIGASHPPQRYNGA 720
Oy 721 INSEFQKAFNCPPNSTNNRGMDSCLRM 749
Db 721 INSEFQKAFNCPPNSTNNRGMDSCLRM 749

RESULT 4
AAB08130
ID AAB08130 standard; Protein: 765 AA.
AC AAB08130;
DE 04-DEC-2000 (first entry)
DI
DX
DY
E A murine neutral endopeptidase metalloproteinase-like enzyme NL-1.
F Nephilysin; neutral endopeptidase metalloproteinase-like enzyme;
G NEP-like enzyme; protein production; protein secretion;
H neurological disease; Alzheimer's disease; pain; psychiatric disorder;
I fertility; bone disease; abnormal phosphate metabolism.
J Mus sp.
K
L
M
N
O
P
Q
R
S
T
U
V
W
X
Y
Z
aa
bb
cc
dd
ee
ff
gg
hh
ii
jj
kk
ll
mm
nn
oo
pp
qq
rr
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uu
vv
ww
xx
yy
zz
AA
BB
CC
DD
EE
FF
GG
HH
II
JJ
KK
LL
MM
NN
OO
PP
QQ
RR
SS
TT
UU
VV
WW
XX
YY
ZZ

```

The present sequence represents a murine neutral endopeptidase metalloproteinase-like enzyme, designated NL-1. The specification also describes NL-2 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active bioproteins, using chimeric constructs containing the foreign protein downstream from and in phase with the N-terminal region. The NL enzymes have been localized to the brain, and may be useful in the treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders. NL enzymes have also been localized to the testis and ovaries, and may be used to control fertility. They have also been localized to bones, and may be used to treat bone diseases, and abnormal phosphate metabolism related to improper peptide processing by the NL-3 enzyme.

Sequence 765 AA;

Query Match 34.8%; Score 1375.5; DB 21; Length 765;  
Best Local Similarity 38.8%; Pred. No. 4.7e-109;  
Matches 295; Conservative 147; Mismatches 267; Indels 51; Gaps 18;

```

Oy 18 GTRIALVVE--VGTLVLTILF-----LYSGLSLQAKOBYCLKEPCIEAAAIL 67
Db 29 GAIVTLGVYSIGKQPLILSLHESWDEKTVYKALDSSLKSDICTPSCVIAARIL 88
Oy 68 SKVNLSDPCDFPFPACDWTISNPIDMPSYGVYVPLRHNVDLKTELKSTSR 127
Db 89 ENMDSDRNCEYFYAGGWLRIHVIPETISRSYVDIIRDELVELIKVLEDSTQHR 148
Oy 128 DTEALAKKILYSSCMNKAIEKADAPLHILHSPRPVLESNIGPQVSWER--K 184
Db 149 --PAVEAKAKTLIRSCMNQSVIEKRDSEPLSVLK--MVGMPVAMDK-----WNETMGLK 199
Oy 185 FSLQTLATFRGQYSNSVFIRLYVSPDKASNEHILKLDQATSLAVREDYLDNSTEAKS 244
Db 200 WELERQALVNLNSQFNRRVLIDLFIMNDQNSRHVYIYDPTLGMMSREYIQOEDNNHK- 258
Oy 245 YKALYKEMVDPAVL-----LGANSRAHDKSVLRLEIKAEIMPEHKESTENYNNKA 297
Db 259 VRKAYLEFMTSVATMLKKDONLSKESAMVEAEVLETHLANVYQERHRHVTALY 318
Oy 298 NKNISELSAM--IPQDMIGYIKKY--IDTRLVPHLDISEPENNVYVVPQFKDLFR 352
Db 319 HRMDLMELQERFGLKGFNMTLFIQNLISVEYELF-----PDERVYVYGYPILENLE 371
Oy 353 ILGSEKRTIANTLVWRMYSTRIPMLSRFRYRMLEFSRVIGTITLLPQMDKCVNFES 412
Db 372 IIDSYSARTMONTLVWRMYSTRIPMLSRFRYRMLEFSRVIGTITLLPQMDKCVNFES 412
Oy 413 ALPYVGVKMFVDYVFOEDKKEEMELVGVRRAPFDMLEKENEMWAGTKRKAARAV 472
Db 432 NMEASVAGSLYIKRAFSDKSTVRELIEKIRSVFQNDDELN--WDESKKRAOEAANI 490
Oy 473 LAKVGYPEFIM--NDFHVEDLKAIFSEADYVGNVLOTRKYLAQSDPFWLRKAVPYTEW 530
Db 491 RQIGYIPDYIILEDNKHIDEYSLSLTFEEDYFENGLOLNKNAQRLKIKREKVDNLM 550
Oy 531 FTNPITYVASTNOIRPAGELOKPFMGTEYPRSLSYGALGYVGHETFGPDNNG 590
Db 551 ITGAAYVNAFYSPNRNQTIVFAGILOPFF--SKQOQSLNFGGIGVIGHETIHGPDNG 609
Oy 591 RYDKNGNLDPMWSTSESEKFKETKCMINQYSNTYWKAGLVNKGKRTIGENINADNG 649
Db 610 RNFDRKNGNLDPMWSTSESEKFKETKCMINQYSNTYWKAGLVNKGKRTIGENINADNG 649
Oy 650 LREAPRAYRKVINDRQGLEPPLPGITTFNNOLFSLAHVACNSYRDEARBOVOIGA 709
Db 670 VQOAVKAYLWMLAD--GKQGRPLGILNLYAQLFFNTVAQWCGSYRDEFAVQISIKTDV 726
Oy 710 HSPQFRYNGAISNSEFQKAFNCPPNSTNNRGMDSCLRM 749
Db 727 HSPKRYVLSLQNTLPGFSEAFHCPRGSPMH--PMKRCRLM 765

```



RESULT 5  
 AAB60562 standard; Protein: 753 AA.  
 XX  
 AC AAB60562;  
 XX  
 DT 27-APR-2001 (first entry)  
 XX  
 DE Human neprilysin-like membrane metalloproteinase SNEPB.  
 XX  
 KW Human; SNEPB; neprilysin-like membrane metalloproteinase;  
 KW splice variant; alternative splicing; zinc endopeptidase family;  
 KW neuropeptide; peptide hormone; processing; metabolism; vaccine;  
 KW drug screening; renal insufficiency; hepatic disease; ischemia; pain;  
 KW hypertension; cancer; inflammation; cardiovascular disease;  
 KW neuronal disease; pancreatic disease; prostatic disease;  
 KW cerebroprotective; hypotensive; cytostatic; antiinflammatory;  
 KW cardiovascular; hepatotropic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1069188-A1.  
 XX  
 PD 17-JAN-2001.  
 XX  
 PF 15-JUL-1999; 99EP-0401767.  
 XX  
 PR 15-JUL-1999; 99EP-0401767.  
 XX  
 PA (SNFT) SANOFI-SYNTHELABO.  
 XX  
 PI Jagerschmidt A, Agnel M, Culouscou J;  
 DR WPT: 2001-212582/22.  
 DR N-PSDB: AAF59660.  
 XX  
 PT New membrane-associated metalloproteinase SNEPB, SNEPB and SNEPC  
 PT polypeptides and polynucleotides, useful for treating e.g. acute and  
 PT chronic renal insufficiency, pain, stroke, cancer, inflammation, renal  
 PT and hepatic ischemia -  
 XX  
 PS Claim 11: Page 33-35; 72pp; English.  
 XX  
 CC The invention relates to the human SNEPB, SNEPB and SNEPC proteins, and  
 CC the cDNAs encoding them. SNEPB, SNEPB and SNEPC are neprilysin-like  
 CC membrane metalloproteinases and are the products of alternative splicing.  
 CC The substrate(s) for the SNEPB proteins are not as yet known, although  
 CC the neprilysin family of zinc endopeptidases play key roles in the  
 CC processing and/or metabolism of neuropeptides and peptide hormones. SNEPB  
 CC nucleotides may be used as hybridisation probes for cDNA and genomic  
 CC DNA; to isolate full-length cDNAs and genomic clones encoding SNEPB,  
 CC SNEPB or SNEPC; to isolate cDNA and genomic clones of SNEPB homologues;  
 CC as research reagents and material for the discovery of treatments and  
 CC diagnostics for animal and human diseases; and for chromosome  
 CC identification. The SNEPB proteins may be used as immunogens to  
 CC produce antibodies immunospecific for SNEPB, SNEPB or SNEPC. Such  
 CC antibodies are used to isolate or identify clones expressing the  
 CC protein, or to purify the proteins by affinity chromatography.  
 CC SNEPB proteins may also be used in screening for compounds which modulate  
 CC SNEPB endopeptidase activity, and to assess enzymatic cleavage of small  
 CC molecule substrates in cells, cell-free preparations, chemical libraries  
 CC and product mixtures. The SNEPB proteins (as vaccine compositions),  
 CC SNEPB nucleotides, and SNEPB activators or inhibitors may be used  
 CC to treat acute and chronic renal insufficiency, renal and hepatic  
 CC ischemia, pain, stroke, hypertensive disease, cancer, inflammation, as  
 CC well as cardiovascular, neuronal, pancreatic, prostatic, renal,  
 CC respiratory or hepatic diseases. They may also be used in modulating  
 CC peptide activation and/or degradation in the brain or kidney or in  
 CC another organ, or to diagnose or treat any disorder related to abnormal  
 CC expression of SNEPB, SNEPB or SNEPC. The present sequence represents

CC SNEPB.  
 XX  
 SQ Sequence 753 AA;  
 XX  
 Query Match 34.4%; Score 1362; DB 22; Length 753;  
 Best Local Similarity 38.6%; Pred. No. 6, 6e-108;  
 Matches 295; Conservative 152; Mismatches 273; Indels 44; Gaps 18;  
 QY 9 VETGKAKR-----GTRALAVYFGVGVLTGLTFLVLSGGLSLQAKQCYCKPCIE 61  
 DB 11 VESAGRAGQKRPGLEGGILLLLTALVALGVLADNRGLPEAOEVEVCTTCQCVI 70  
 QY 62 AAAAILSKVNLSPDCNFFERACDGIISNPPEDMPISYGVYPMIRHNDLKLLEK 121  
 DB 71 AAARILQMDPTTEPCDFYFAGCGMLRRVPEIETSRFSIFVLDLEVLILKAVLEN 130  
 QY 122 SISRRDTEALQAKILYSSCMNEKALEKADAKLLILHRSPPRWVLSNIGPEVWS 161  
 DB 131 STA-KDPAVEKAKATILYRSCMNOSVIEKRSQPLDIL-EVGGWVYAMDR-----WN 181  
 QY 182 ER---KESLQTLATFFRGQYNSVFIRLYSPDDKASNEHILKIDQATLSLAVREDYLDN 238  
 DB 182 ETVGLEWELERQALMNSQFNRRVILDFINDDQNSRHIIYIDQPLGMPSEYFENG 241  
 QY 239 STEAKSYRDALYKFWDTAVLL--GANSR---AEHDKSVYLRLEIKIETIPIHENRT 292  
 DB 242 GSNRK-VREAYLQFVSVATLLREDANLPDSCLVQEDMVQVLETLQAKATVPOEERH 300  
 QY 293 SE-AMYNKKNISLSAM--IQFQDLGYIKKVIDTRILYPLHK-DISPESENVVHVPQYK 348  
 DB 301 DVIALYHRMGLELQSGFGLGFWTLTQYVLS-----VKILPDEEVYVIGPIPLQ 355  
 QY 349 DLFRIIGSEKRTIANYLWVWVYSRIPLNSRFQYRWLEESRVLTGTTLLPQDKCVN 408  
 DB 356 NLENIIIDYTSARTIONLYWRLVLDRIQSLQRFQDTRVNYRKALFCTMVEEVRRECVC 415  
 QY 409 FTESALPYVVGKMEVDYVFOEDKEMEMELVGVYMAFLDMKEKEMMDAGTKKAKK 468  
 DB 416 YVNSNMENAVGSLYVREAFPGDSKSNVRELIDKVTVEVETLD-BLGWMDSESKKAKQEK 474  
 QY 469 ARAVLAKVGYPEFINMDT--VNEIDKAIKFEADYFGVNLQTRKYLQSDFFWLKRAVP 526  
 DB 475 AMSIRQIGHPDYILEETRRRLDEEYSNLFSEDLTFENSLNKLAVGQSR.LRKREKVD 534  
 QY 527 KTEMFTNPTTVNAFYVSASTNQIRPAGELQKPEFMEGTVEPRSLSGALGVYGHFTGFE 586  
 DB 535 PNMIIIGAAVNAFYSPNRNOIYFPAIILQPEFF-SKEQPOLNFGIGMTVGHETGFE 593  
 QY 587 DNNGRKYDKNGNIDPMWSTSEBEKFEKTKKMINOVSNYWKAG-LNYGKRTIGENIA 645  
 DB 594 DDNGRNEFDKNGNMDWSNFSQHFRESECMYIOIGNTSWDLADBNVNGENTIGENIA 653  
 QY 646 DNGLEAFAYRKWINDRQGLEBPLPGITFTNNQLEFLSYAHVRCNSYPPAAREOV 705  
 DB 654 DNGGVQAYKAYLKW---AEQKQDQLGDLTDHQLDFINVAQWCSYPERFALOSI 710  
 QY 706 QIASHSPQFQNGCAISNEEPKAKNCPNPSIMNMGMSCRUM 749  
 DB 711 KTVVHSPKRYVLSLQNLAAFDTRFCARGTDM-PKRCRCRW 753  
 RESULT 6  
 AAB83842 standard; Protein: 753 AA.  
 XX  
 AC AAB83842;  
 XX  
 DT 23-JUL-2001 (first entry)  
 XX  
 DE Amino acid sequence of a human metalloproteinase enzyme IG5.  
 XX  
 KW Metalloproteinase; IG5; infection; pain; cancer; diabetes; obesity;  
 KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;

KW	hypertension; hypertension; urinary retention; osteoporosis;
KW	angina pectoris; myocardial infarction; stroke; ulcer; allergy;
KW	benign prostatic hypertrophy; migraine; psychotic disorder;
KW	neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
KW	neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
KW	cardiovascular disease; arteriosclerosis; cerebrovasospasm;
KW	subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
KW	peripheral vascular disease; Raynaud's disease; motility disorder;
KW	gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
KW	inflammation; chemotherapy induced injury; tumour invasion;
KW	immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
KW	severe mental retardation; dyskinesia; Huntington's disease;
KW	Gilles de la Tourette's syndrome.
OS	Homo sapiens.
XX	
PN	WO200136610-A1.
XX	
PD	25-MAY-2001.
XX	
XX	17-NOV-2000; 2000MO-EPI1532.
XX	
PR	19-NOV-1999; 99EP-0203662.
PR	19-NOV-1999; 99NL-1013616.
PR	31-MAY-2000; 2000EP-0201937.
PR	31-MAY-2000; 2000NL-1015356.
XX	
PA	(SOLV ) SOLVAY PHARM BV.
XX	
PI	Deleersnyder W, Wiegers R, Weske M;
XX	
DR	WPI: 2001-343815/36.
DR	N-PSDB: AAF89739.
XX	
PT	New IGSS polypeptides useful for treating infections, pain, cancer,
PT	diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
PT	hypertension, urinary retention and Parkinson's disease
XX	
PS	Claim 3: Page 9-10; 115pp; English.
XX	
CC	The present sequence represents a human metalloprotease enzyme designated
CC	IGSS. IGSS polynucleotides and polypeptides are useful for treating
CC	infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
CC	Parkinson's disease, acute heart failure, hypertension,
CC	urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC	stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
CC	psychotic and neurological disorders, autism, multiple sclerosis,
CC	Alzheimer's disease, and other neurodegenerative diseases, sleep
CC	disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
CC	cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
CC	infarction, peripheral vascular disease, Raynaud's disease, kidney
CC	diseases, gastrointestinal disorders, motility disorders and conditions
CC	of delayed gastric emptying, post-operative or diabetic gastroparesis,
CC	diarrhoea, inflammations, chemotherapy induced injury, tumour invasion,
CC	immune disorders, arthritis, endotoxin shock, sepsis, complications of
CC	diabetes mellitus, and severe mental retardation and dyskinesias, such
CC	as Huntington's disease or Gilles de la Tourette's syndrome.
XX	
SO	Sequence 753 AA:
XX	
QY	Query Match 34.2%; Score 1352; DB 22; Length 753;
XX	Best Local Similarity 38.4%; Pred. No. 4,8e-107;
XX	Matches 293; Conservative 153; Mismatches 274; Indels 44; Gaps 18;
DB	
11	9 VENGKANKR-----GTRIALVYVGGTLVGLTFLVSGILSTIAKQETCKREKIE 61
DB	11 VESAGRGQGRPFLEGGILLILLYTALVALVAGLVADRGRIGPEAEQVSEVCTPGCVI 70
QY	62 AAAAISLTKLVSDPCDNFFRFACGQSNNDIPEDMNSVYVWMLAHNDLAKELER 121
DB	71 AAARITLQNDPTPEDDDFYQFACGWLKRRIYVETPNSRISIFVLELDEVLTKAVLEN 130
QY	122 SISRRODTAIOAKILVSSCMNEKAIEKADKPLHLIRHSPFWFVYSNIGPGWMS 181

Db 131 STA--KORPAVEKARILYRSCNMQSVIERKSGPPLILDI-EVYGGWPAAMD-----WN 183  
 182 ER---KRSLLQTLATRGQYSNSVFTRLYVSPDDRKASNEHLIKLDAOTLSLAVEDYLDN 236  
 Db 182 EYGLELELELROLALNNSQFNRRVLLIDLEIMWDDQNSRHITYIDQPTLGPMSREYFNG 241  
 QY 239 STEAKSYRDLAYKFMVDTAVLL--GANSR-----AEHMKSVLRLEIKIAIMPHENRT 292  
 Db 242 GSNRK-VREAYILQFMVSATLLREDANLPRDSCLOEDMMOYLELEIOLAKATVPOEERH 300  
 QY 293 SE-AMNKNMISLSM--IPQEDMGLTKKVIDRLYPLHK-DISPENVVVRPOYFK 348  
 Db 301 DVALTHRRGLEELQSQFGLKGFNMNTLFIQYLS-----VKILLPDEEVVYGYPIYLQ 355  
 QY 349 DFRILGSEKKTIANYLVWRYVYSRIPYLSRPFQRYLWLESRYLGTTLLPQMDKCVN 408  
 Db 356 NLENIIDTYSARIQYLVWRLYDLRIGLSLQRFEDTIVNRKALFETIMVEYWRKCVG 415  
 QY 409 FTSALPYYVVGKMFVDYVFOEKKKMEBELVEGVMAFIDMLEKENEMDAGTKRKAKK 468  
 Db 416 YVNSNMENAVGSLYVREAPGDSKSMVELIDKRVTFVEFLD-ELGMDSESKKQOEK 474  
 QY 469 ARAVLAKVYGFPEFINMDTH--VNEDLKAIKFSADYGVNYLQTRKYLAAQSDFMWRKAP 526  
 Db 475 AMSIRQIHPDYILLENNRRLDEYSYLNSESDLYEENSQNLKVAQASLKRLEKVD 534  
 QY 527 KTEWFTNPITYVAFTSASNOIRPAGELQKPFWTGTEYPRSLSYAGIVYGHETFG 586  
 Db 535 PMLWITGAIVNAVAFSPRRNDIIVPAGLIOPPF-SKEQDPAIFGIGVIGHETFG 593  
 QY 587 DNNGRKYDKNGMLDPMWSTEESEKFEKTKCMINQYSNYWKRAG-LNYGKRTLGENT 645  
 Db 594 DONGRNFDPKNGMDWMSNFSTQHRRESECMITQYCNYSMDLADQNVANGFTLENTA 653  
 QY 646 DNGGRLRFAFRYARKINDRRGCLLEPLLPGITTTNNOLFPLSYAHVRCNSYREARRECV 705  
 Db 654 DNGGKQKATKALKM--AAGGKDQQLPGIDLTHEOLFPIINAQVWCSGYRPEFAIOSI 710  
 QY 706 QIGASHPPQFRVNGAISNSEFOKAFNCPPNSVTWNRGMDSCRLM 749  
 Db 711 KTDVHSPLEKRYVLSQLWLAFAFDTPCANGTGMH-PKECRWV 753  
 RESULT 7  
 AAY44177  
 ID AAY44177 standard; Protein; 774 AA.  
 XX  
 AC AAY44177;  
 XX  
 DT 01-FEB-2000 (first entry)  
 XX  
 DE Rat membrane metalloprotease NEPII protein.  
 XX  
 KW Rat; membrane metalloprotease; neprilysin II; NEPII; inactivation;  
 KW neuron; hormone; peptide messenger; inhibitor; detection; disorder;  
 KW cardiovascular disease; neurodegenerative disease; growth disorder;  
 KW hypothalamic-hypophyseal axis; endocrine disorder.  
 XX  
 OS Rattus rattus.  
 XX  
 PN FR2777291-AL.  
 XX  
 PD 15-OCT-1999.  
 XX  
 PF 08-APR-1998; 98ER-0004389.  
 XX  
 PR 08-APR-1998; 98ER-0004389.  
 XX  
 PA (INRA ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PI Ouimet T, Gros C, Haret C, Bonhomme MC, Facchinetti P,  
 PI Schwartz JC;

XX WPI: 1999-593429/51.  
 DR N-PSDB: AAZ28810.  
 XX New membrane metalloprotease NEP II, involved in proteolysis of  
 PT neuronal and hormonal peptides, used to screen for inhibitors,  
 PT potentially useful for treating e.g. cardiovascular disease  
 XX  
 PS Claim 1: Page 12-16; 29pp; French.  
 XX  
 CC This sequence represents the rat membrane metalloprotease designated  
 CC neprilysin II (NEPII), which is involved in (in)activation of neuronal  
 CC and hormonal peptide messengers. NEPII is used to screen for specific  
 CC substrates (used to detect NEPII in cells and tissues) or inhibitors,  
 CC which can also be used to detect NEPII or for treatment of disorders  
 CC related to peptidergic signalling in which NEPII is involved, e.g.  
 CC cardiovascular or neurodegenerative diseases; growth disorders of  
 CC endocrine origin; disturbances of the hypothalamic-hypophyseal axis  
 CC or endocrine disorders.  
 CC  
 XX Sequence 774 AA:  
 SQ  
 Query Match 34.1%; Score 1351; DB 20; Length 774;  
 Best Local Similarity 38.2%; Pred. No. 6.1e-107; Indels 46; Gaps 18;  
 Matches 289; Conservative 156; Mismatches 266;  
 QY 18 CTRIALVVF--VGGLT-VLGTILE-----LYSGGLLSIAQKQECYCLKPECIEAAAIL 67  
 DB 39 GAITLVGVYSIGKQLPLNSLHVSHERTVKRVLRDSSQKSDICTPSCVIAAARLL 98  
 QY 68 SKVNLSDPCDNFERRACDWMISNPIEDMPSGYPMRHNVDLKELEKISRRR 127  
 DB 99 QNMQSKPCDNFQYACGGLRHVHPENSRYSVFLIDLELYLKVLEDDSSVQHR 158  
 QY 128 DTEAOKKILYSSCMNEKATEKADAPLHLHSPFRWPVLESNIGPEGVSR--K 184  
 DB 159 --PAVEKAKTLYRSCMNSVLEKRDSEPLNVL--DMTGMVPAADK-----WNETGPK 209  
 QY 185 FSLQTLATFRGOYSNSVFIHLYVSPDKASNEHILKIDATLSLAVREDYLDNSTAKS 244  
 DB 210 WELERQLAVLNSQFRRLVIDLFIWMDQNSRHVYIIDQTLMPREYTF--KEDSHR 267  
 QY 245 YDALKYKENVDAVL-----IGANSRAEDMKSVLELEKIAEIMPHENRYS--BMY 297  
 DB 268 VREAYLQFTSVATMLRDNLPGFTDLVQEMAOVLHEHLINATYPOKRRIDYALY 327  
 QY 298 NKNMISELSAM--IPOFDMLGYIKKVIDTRYPLKDISPSENVVVRVYQFKDLRLIG 355  
 DB 328 HRNGLELDGRGKLGKFNMTLFTQNLVLSVQV---ELLPMEEVYVYGIPYLENLEIID 383  
 QY 356 SEERKTIANTLVWRYVSKIPULSRFOYRMLEFSRVIOGTTLLPQMDKCVNFIESALP 415  
 DB 384 VEPAGTLQNLVWRLVLDIGLSIQFKEARVDYKALGITMEVNRRECVSYNSMME 443  
 QY 416 YVVGKKEVDVYFOEDKKEEMEEVEGVRAWFIDMLEKENEMWDACTKKAKKAPAYLAK 475  
 DB 444 SAVGSLIKAFSKDSKISYSELIEKIRSVFVNDIDELN--WMDDESKKKAQKALNIEQ 502  
 QY 476 VGYPEFTM--NDTHVNEDLKAFSEADYFGNVLQTRKTLASDFMLKAPKTEMTFN 533  
 DB 503 IGYDDYILLEDNHNRHDEEVSLSLTFENLQNLKNNRQSLKLLEKQDQNMILIG 562  
 QY 534 PTYNATYASTNOIRPAGELOKPFEGWTEYPRSLSYGAIYGVHEFTFGDNGRKY 593  
 DB 563 AAVNATYSPRRNLIYPAIILQPPF--SKDQDALNFGSIGVIGHETTHGDDGRNF 621  
 QY 594 DKNGLDPMWSTSESEKFKETKCMINQYNYWYKKA--GLNYGKRTLENTADNGLRE 652  
 DB 622 DKNGMLDMWNSFARHFRQSQCMYQYNSFMEIADNQNNGVSTLGTENIDNGCYAQ 681  
 QY 653 AFRAARKVINDRQGLEPILLPGITFTNNQLFELSYAHVNCNSYREAPAREQYOGASH 712  
 DB 682 AYKATLQNL---ABSGRQRLPGILNTYADLFINTAYQWCGSVRPFALQSIKTIVHSP 738

QY 713 POFVNGAISNSEFQKAFNCPSNTMNGMDSCLRW 749  
 DB 739 LKRYVLSLQNLPGFSEAFHCPGSPMH--PANKRRIRW 774  
 RESULT 8  
 ID AAB60561  
 XX AAB60561 standard; Protein: 779 AA.  
 AC  
 XX  
 XX  
 DE 27-APR-2001 (first entry)  
 XX  
 XX Human neprilysin-like membrane metalloprotease SNEPa.  
 XX  
 XX Human: SNEPa; neprilysin-like membrane metalloprotease;  
 KW splice variant; alternative splicing; zinc endopeptidase family;  
 KW neuropeptide; peptide hormone; processing; metabolism; vaccine;  
 KW drug screening; renal insufficiency; hepatic disease; jaundice; pain;  
 KW hypertension; cancer; inflammation; cardiovascular disease;  
 KW neuronal disease; pancreatic disease; prostatic disease;  
 KW respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;  
 KW cerebroprotective; hypotensive; cytostatic; antiinflammatory;  
 KW cardiovascular; hepatotropic.  
 OS Homo sapiens.  
 XX  
 XX EPI069188-A1.  
 PN 17-JAN-2001.  
 PD 15-JUL-1999; 99EP-0401767.  
 PF 15-JUL-1999; 99EP-0401767.  
 PR 15-JUL-1999; 99EP-0401767.  
 PA (SNF1) SANOFI-SYNTHELABO.  
 XX  
 XX Jagerschmidt A, Agnel M, Culouscou J;  
 PI WPI: 2001-212582/22.  
 DR N-PSDB: AAF59659.  
 XX  
 PT New membrane-associated metalloprotease SNEPa, SNEPb and SNEPc  
 PT polypeptides and polynucleotides, useful for treating e.g. acute and  
 PT chronic renal insufficiency, pain, stroke, cancer, inflammation, renal  
 PT and hepatic ischemia  
 PS Claim 11; Page 28-30; 72pp; English.  
 XX  
 XX The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and  
 XX the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like  
 XX membrane metalloproteases and are the products of alternative splicing.  
 XX The substrate(s) for the SNEP proteins are not as yet known, although  
 XX the neprilysin family of zinc endopeptidases play key roles in the  
 XX processing and/or metabolism of neuropeptides and peptide hormones. SNEP  
 XX nucleotides may be used as hybridisation probes for cDNA and genomic  
 XX DNA; to isolate full-length cDNAs and genomic clones of SNEP homologues;  
 XX SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues;  
 XX as research reagents and material for the discovery of treatments and  
 XX diagnostics for animal and human diseases; and for chromosome  
 XX identification. The SNEP proteins may be used as immunogens to  
 XX produce antibodies immunospecific for SNEPa, SNEPb or SNEPc. Such  
 XX antibodies are used to isolate or identify clones expressing the  
 XX protein, or to purify the proteins by affinity chromatography.  
 XX SNEP proteins may also be used in screening for compounds which modulate  
 XX SNEP endopeptidase activity, and to assess enzymatic cleavage of small  
 XX molecule substrates in cells, cell-free preparations, chemical libraries  
 XX and product mixtures. The SNEP proteins (as vaccine compositions),  
 XX SNEP nucleotides, and SNEP activators or inhibitors may be used  
 XX to treat acute and chronic renal insufficiency, renal and hepatic  
 XX ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as  
 XX well as cardiovascular, neuronal, pancreatic, prostatic, renal,

CC respiratory or hepatic diseases, they may also be used in modulating  
CC peptide activation and/or degradation in the brain or kidney or in  
CC another organ, or to diagnose or treat any disorder related to abnormal  
CC expression of SNEPA, SNEP or SNEPC. The present sequence represents  
CC SNEPA.  
XX

SO Sequence 779 AA;

Query Match 33.9%; Score 1343.5; DB 22; Length 779;  
Best Local Similarity 39.5%; Pred. No. 2.7e-106;  
Matches 286; Conservative 144; Mismatches 258; Indels 37; Gaps 17;

```

OY 42 OGLSLQAKOEYCLKPECIAAAILSKVNLSDPCDNFFRACDGMISNNIPEDMSY 101
DB 77 RGIPDAOESEVCTTGCYTAARILQNDPTEPCDDYQACGGLRRHVIPETNSRY 136
OY 102 GYVPMLRHNVDLKLKELLESISRDRDEAIQAKILYSSCMNEKAIEKADAKPILHLR 161
DB 137 SIFDVLRLDEVLKAVLENSTRA--KDRPAVKANTLVKSCMNQSVIEKRSQPLDIL- 193
OY 162 HSPFRPVLSEINIGPEGWSE--KFSLLQTLATFRQYSNSVFRILYSPDKASNEH 218
DB 194 EYVGVPVAMDR-----WNETVGLLEWELERQLALMSQFRRVILDLFINDDQNSRH 247
OY 219 IILKIDQATSLAVREDYLDNSTEAKSYRDALYKFWDTAVLL--GANSR---AEHDMK 272
DB 248 IYIDOPTIGMSREYFRNGSNRK--VEAYLQFVSVATLLRDANLPRDSCVLQEDMV 306
OY 273 SVLRLEIKAEITMIPHENTSE--AMYNKMNISELSAM--IPQMDLYIKKVIDTRLYPH 329
DB 307 QVLELETLQAKATVPOEERHVDIALYHRMGLQSOGLKGPMTLFTQVLSS----- 361
OY 330 LR-DISPENVVVRVPOFKDLFRIGSEKKTATLVWRMYVSRIPNLSRRROYRWLE 388
DB 362 VKIKLLPDEEVVYVGIPLQWLENIIDYISAKITQNTLVWRVLDRIQSLSQRFKPTRVY 421
OY 389 FSRVIGCTTTLLPOMDKCVNFIESALPYVVKMEVDYVFOEDKKEMMEELVEGVRAFD 448
DB 422 YRKALFGTMEVEVWRRCVGVNSNMENAVSLYVREAFPGDSKSNARELIDVRYVEYE 481
OY 449 MLERENEMDAGTRKAKERAKAVLAVGVPEELMDTH--VEDDKAIKFEADYFGNV 506
DB 482 TLD-ELGMDSESKKAKQEKAKMSRDIQGHDPDYLLEETNRKRLDEEYSNLFSEDLTFENS 540
OY 507 LOTKKYLAOSDFEFLKRAVKTETFTNPTVNAFASASTNQLFRPAGELQKPEFGTEP 566
DB 541 LQNLKVAQSRSLRKLRKREKVDPMIIGAAVNAFYSPNNQYVFRAGILQPPFF-SKEOP 599
OY 567 RSLSYGAIGYVGFHEFGDNNGRKYDKNGNLDPWMSSTESEKREKTKCMINOSNY 626
DB 600 QALNFGSIGVIGHETTHGFDDNGRFEDNGNMNMWMSNFSTQHFREDOSECMIYQGNYS 659
OY 627 WKKAG--LVNKGKTTGTENIADNGLEAFRAVRKVIINDRQGLLEPLLGITFTNNOLEF 685
DB 660 WDLADQWNGEFTLTGENIADNGVRAQAKALKMM---AEGKKQOQJPGDLTHEDLEF 716
OY 686 LSYAHRCSYSPREARVOYGASPPQFRVNGAISSEEFQAFNCPPNSTNRGMD 745
DB 717 INAQWCSSTYPERAIOISIKTIDVSPKRYVLSIQMLAFAFDTFHCAKRTPMH-EKER 775
OY 746 CRIM 749
DB 776 CRVM 779

```

RESULT 9  
AAB83841  
ID AAB83841 standard; Protein: 779 AA.

XX AAB83841;  
XX 23-JUL-2001 (first entry)

DE Amino acid sequence of a human metalloprotease enzyme IG55.  
XX  
XX Metalloprotease; IG55, infection; pain; cancer; diabetes; obesity;  
XX anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;  
XX hypotension; hypertension; urinary retention; osteoporosis;  
XX benign prostatic hyperplasia; stroke; ulcer; allergy;  
XX neurological disorder; autism; multiple sclerosis; Alzheimer's disease;  
XX neurodegenerative disease; sleep disorder; epilepsy; kidney disease;  
XX cardiovascular disease; arteriosclerosis; cerebrovasospasm;  
XX subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;  
XX peripheral vascular disease; Raynaud's disease; motility disorder;  
XX gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;  
XX inflammation; chemotherapy induced injury; tumour invasion;  
XX immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;  
XX severe mental retardation; dyskinesia; Huntington's disease;  
XX Gilles de la Tourette's syndrome.

Homo sapiens.

WO200136610-A1.

25-MAY-2001.

17-NOV-2000; 2000WO-EP11532.

19-NOV-1999; 99EP-0203862.

19-NOV-1999; 99NL-1013616.

31-MAY-2000; 2000EP-0201937.

31-MAY-2000; 2000NL-1015356.

(SOLV) SOLVAY PHARM BV.

DeJersnijder W, Wieggers R, Weske M;

WPI; 2001-343815/36.

N-PSDB; AAF89738.

New IG55 polypeptides useful for treating infections, pain, cancer,

PT diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,

PS hypertension, urinary retention and Parkinson's disease

XX Claim 3; Page 8; 115pp; English.

XX The present sequence represents a human metalloprotease enzyme designated  
XX IG55. IG55 polynucleotides and polypeptides are useful for treating  
XX infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,  
XX Parkinson's disease, acute heart failure, hypotension, hypertension,  
XX urinary retention, osteoporosis, angina pectoris, myocardial infarction,  
XX stroke, ulcers, allergies, benign prostatic hyperplasia, migraine,  
XX psychotic and neurological disorders, autism, multiple sclerosis,  
XX Alzheimer's disease, and other neurodegenerative diseases, sleep  
XX disorder, epilepsy, cardiovascular diseases, arteriosclerosis,  
XX cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral  
XX infarction, peripheral vascular disease, Raynaud's disease, kidney  
XX diseases, gastrointestinal disorders, motility disorders and conditions  
XX of delayed gastric emptying, post-operative or diabetic gastroparesis,  
XX diarrhoea, inflammation, chemotherapy induced injury, tumour invasion,  
XX immune disorders, arthritis, endotoxin shock, sepsis, complications of  
XX diabetes mellitus, and severe mental retardation and dyskinesias, such  
XX as Huntington's disease or Gilles de la Tourette's syndrome.

SO Sequence 779 AA;

Query Match 33.7%; Score 1333.5; DB 22; Length 779;  
Best Local Similarity 39.2%; Pred. No. 2e-105;  
Matches 284; Conservative 145; Mismatches 258; Indels 37; Gaps 17;

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OY 42 OGLSLQAKOEYCLKPECIAAAILSKVNLSDPCDNFFRACDGMISNNIPEDMSY 101
DB 77 RGIPDAOESEVCTTGCYTAARILQNDPTEPCDDYQACGGLRRHVIPETNSRY 136
OY 102 GYVPMLRHNVDLKLKELLESISRDRDEAIQAKILYSSCMNEKAIEKADAKPILHLR 161

```



QY 627 WKAG-LNVKGRITLGINADNGSLREAFRAKRWINDROGLEPILPITITNNOLF 685  
 Db 651 WDLADEQVNGVFNLTGENDNGSVRAKAYLKWM--AEGKDOQLPGLDTHQLEFF 707  
 QY 686 LSTAHVRCNSYRPPAREQVGAHSPPOFRVNGAISNSEEFQAKFNCPPNSTNRGMD 745  
 Db 708 INVAQVWCGSYRPEFAIOSIKTVHSPKRYVLSQNLAAFAFDTFHCANGTMMH-PKER 766  
 QY 746 CRLW 749  
 Db 767 CRW 770

RESULT 11  
 ABB79521 standard; Protein; 779 AA.  
 ID ABB79521  
 XX ABB79521:  
 AC 23-SEP-2002 (first entry)  
 XX Human SEP endopeptidase.  
 DE Human SEP endopeptidase.  
 XX SEP: endopeptidase; enzyme; human; neuropeptide Y1, receptor;  
 KM male sexual dysfunction; male erectile dysfunction; obesity;  
 KW anorexia; bulimia; vasotropic; anorectic; therapy; inhibitor.  
 OS Homo sapiens.  
 XX MO200247670-A1.  
 PN 20-JUN-2002.  
 PD 10-DEC-2001; 2001WO-1B02399.  
 XX 15-DEC-2000; 2000GB-0030647.  
 PR 06-APR-2001; 2001GB-0008730.  
 PR 23-APR-2001; 2001GB-0009910.  
 PR 04-MAY-2001; 2001GB-0011037.  
 PR 29-JUN-2001; 2001US-0895367.  
 PR 13-JUL-2001; 2001US-0905846.  
 PR 24-AUG-2001; 2001GB-0020679.  
 XX (PFITZ ) PFIZER LTD.  
 PA (PFITZ ) PFIZER INC.  
 XX Naylor AM, Van Der Graaf PH, Wayman CP;  
 PI WPI: 2002-547828/58.  
 DR N-PSDB; ABB84279, ABB84280.  
 DR Use of an inhibitor of neuropeptide Y in the preparation of medicament  
 PT for the treatment or prevention of male erectile dysfunction  
 XX Disclosure: Fig 9; 17pp; English.  
 PS The present sequence is the protein sequence of human SEP, a  
 CC soluble secreted endopeptidase. The invention relates to the use  
 CC of an inhibitor of NPY, or an inhibitor of NPY Y1 receptor,  
 CC especially an inhibitor selective for an NPY or NPY Y1 receptor  
 CC associated with male genitalia, in the preparation of a medicament  
 CC for the treatment or prevention of male sexual dysfunction,  
 CC especially male erectile dysfunction (MED). The NPY inhibitor  
 CC may be used with an auxiliary active agent such as an SEP  
 CC inhibitor. The invention provides an assay that can be used to  
 CC detect candidate inhibitors of SEP. In addition to treatment of  
 CC MED, NPY inhibitors can also be used to treat abnormal drink and  
 CC food intake disorders, such as obesity, bulimia, anorexia and  
 CC metabolic disorders.  
 CC Sequence 779 AA;

Query Match 33.7%; Score 1332.5; DB 23; Length 779;  
 Best Local Similarity 39.2%; Pred. No. 2.4e-105;  
 Matches 284; Conservative 145; Mismatches 258; Indels 37; Gaps 17;

QY 42 OGLSLQAKQECYCLKPECIEAAATILSKVNSVDCDNEFFRACGMSNNPDEMP 101  
 Db 77 KGIPEAQEVESECTTGGVIAAARILQNNDDPTTECDDEYFACGGMRRVHETNSR 136  
 QY 102 GYVPMLRNHNVDLKLKLEKLSRRRDTEATOKATILVSSCNEKAIEKADKPLHLR 161  
 Db 137 SIFDVLRLDELVIYILKAVLENSTA--KDRPAYEKATILVRSQMSVIERSSQPLDIL 193  
 QY 162 HSPFRPVLSESVIGPEGWSER--KESLQTLATFRGOYSNVPILRYSPDDKASNEH 218  
 Db 194 EYVGGPVPAMDR-----WNETVGLLEWLEQLALMNSQFNRRVILIDFIWNDQNSRH 247  
 QY 219 ILKLDQATLSLAVREDYLDNSTEAKSYDALYKFWVDYAVLL--GANSR-----AEDMK 272  
 Db 248 IYIDQPTLGMPSREYTYNGSNRK-VREAYLQFVSVATILREDANPRDCLVQEDMV 306  
 QY 273 SYLLEIKIATIMIPHENRIS-AMYNKMNISESAM--IPQDWLGIKKVIDTRLYPH 329  
 Db 307 QYLELETLQAKATVQOEERHVDVIALYHRMGLLELOSQGLKGFNWTLFIQTVLSS----- 361  
 QY 330 LK-DISEPENVYVRYPOYFKDLFRIGSERKKTANTLYMAMYSRIPINSRRQYMLE 388  
 Db 362 VKIKLPPDEYVYVGIPIQLMLENIDITYSAKTQNLVWLVLVDRIGSLSORERKDRVN 421  
 QY 389 FSRVIGTFTTLLPQWDCVNEFESALPYVVGKMFVDYVFOEDKKNMEELVEGVRAFI 448  
 Db 422 YRKALFTGTVEEVWRRECQVGVYNSNMENAVGSLYREAFPGDSKSMRELIDRYVFE 481  
 QY 449 MLEKENEMWADGTRKRAKRAKARAVLAVGYREPIANDTH--VNEDKAIFSEADYFGNV 506  
 Db 482 TLID-ELGMDESKKKAQEKASIREQIGHDPDYLEEMNRRLDEEYSLNFSDELFEYS 540  
 QY 507 LOTRKYLAOSDFWLRKRAVPTKEFTNPTVNAFYASASTNOIRPPGELQKPPFWGTEP 566  
 Db 541 LONLKVGQNSRLKRLREKVDPNMLIIIGAAYVNAFYSPNRQIYFPACIILPPEF-SKEOP 599  
 QY 567 RSLSTGALGYVGHFTHGPDNNGKRYDKNGNIDPMWSTSESEKFEKTKCMATQYSNYY 626  
 Db 600 QALNFGGIGMVTGHEITHGPDNNGKNGNMDMWSNFSQHFREQSCMTIYQYNS 659  
 QY 627 WKAG-LNVKGRITLGINADNGSLREAFRAKRWINDROGLEPILPITITNNOLF 685  
 Db 660 WDLADEQVNGVFNLTGENDNGSVRAKAYLKWM--AEGKDOQLPGLDTHQLEFF 716  
 QY 686 LSTAHVRCNSYRPPAREQVGAHSPPOFRVNGAISNSEEFQAKFNCPPNSTNRGMD 745  
 Db 717 INVAQVWCGSYRPEFAIOSIKTVHSPKRYVLSQNLAAFAFDTFHCANGTMMH-PKER 775  
 QY 746 CRLW 749  
 Db 776 CRW 779

RESULT 12  
 AAU78850 standard; Protein; 779 AA.  
 ID AAU78850  
 XX AAU78850:  
 AC 18-JUN-2002 (first entry)  
 XX Novel neprilysin family protein, 56638.  
 DE Neprilysin family; human; gene therapy; protein therapy; vaccine;  
 KW neprilysin protease; pain; pain associated disorder; tissue injury;  
 KW chest pain; complex regional pain syndrome; CRPS; headache; migraine;  
 KW reflex sympathetic dystrophy; RSD; tooth pain; musculoskeletal disorder;  
 KW joint pain; surgery; inflammation; irritable bowel syndrome; anaemia;  
 KW aberrant spermatid cell activity; infertility; cancer; brain disorder;









QY 459 AGTKAKAKARAVLAKVGYPEFLMNDTH--VNEDLAKIKSEADYFGNVLQTRKTLAOS 516  
 Db 414 ESKKKAQEKAMSIREDQGHDIYLEEMNRRLDEESNLNFSDDLFEENSLQMLKYGAGR 473  
 QY 517 DFWLRKAVPKTEFTPTNPTNAFYSASTNOIRPAGLELOKPFMGTEYPRSLSYGATGV 576  
 Db 474 SLRKLRKAVPKTEFTPTNPTNAFYSASTNOIRPAGLELOKPFMGTEYPRSLSYGATGV 576  
 QY 577 IVGHEFTHGFDNNGRKDYKNGNDLPMWSTSESEKFEKTKCMINQYSNTYWKAG-LNVK 635  
 Db 533 VIGHEITHGDDNCRNDRDKNGNMWMSNFSTQHFREOSECMITQYGNYSMDLADQONV 592  
 QY 636 GKRTLGENDNGGLREAFRAKRWINDRROGLEEPLLPITFTNNQLEFLSYAHRCMS 695  
 Db 593 GFNTLGENIADNGCVRAQYKAYLKKM--AEGKQDQLPGLDITHTQLEFTINAYQWCS 649  
 QY 696 YRPFARQVOIGAHSPQPRVNGAISNSEFOKAFNCPNSTNMNGMSCLM 749  
 Db 650 YRPFARQVOIGAHSPQPRVNGAISNSEFOKAFNCPNSTNMNGMSCLM 749

RESULT 15  
 AAB83840

ID AAB83840 standard; Protein: 691 AA.

XX AAB83840;

XX 23-JUL-2001 (first entry)

DE Amino acid sequence of a human metalloprotease enzyme IG55.

XX Metalloprotease; IG55; infection; pain; cancer; diabetes; obesity;  
 KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;  
 KW hypertension; hypertension; urinary retention; osteoporosis;  
 KW angina pectoris; myocardial infarction; stroke; ulcer; allergy;  
 KW benign prostatic hyperplasia; migraine; psychotic disorder;  
 KW neurological disorder; autism; multiple sclerosis; Alzheimer's disease;  
 KW neurodegenerative disease; sleep disorder; epilepsy; kidney disease;  
 KW cardiovascular disease; arteriosclerosis; cerebrovasospasm;  
 KW subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;  
 KW peripheral vascular disease; Raynaud's disease; motility disorder;  
 KW gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;  
 KW inflammation; chemotherapy induced injury; tumor invasion;  
 KW immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;  
 KW severe mental retardation; dyskinesia; Huntington's disease;  
 KW Gilles de la Tourette's syndrome.

OS Homo sapiens.

XX WO200136610-A1.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-EPI1532.

XX 19-NOV-1999; 99EP-0203862.

XX 19-NOV-1999; 99NL-1013616.

XX 31-MAY-2000; 2000EP-0201937.

XX 31-MAY-2000; 2000NL-1015356.

XX (SOLV ) SOLVAY PHARM BV.

XX Deleersnyder W, Wieggers R, Weske M;

XX WPI, 2001-343815/36.

XX N-PSDB; AAF89737.

XX New IG55 polypeptides useful for treating infections, pain, cancer,  
 PT diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,  
 PT hypertension, urinary retention and Parkinson's disease  
 XX Claim 3; Page 6; 115pp; English.

CC The present sequence represents a human metalloprotease enzyme designated  
 CC IG55. IG55 polynucleotides and polypeptides are useful for treating  
 CC infections, pain, cancer, diabetes, Obesity, anorexia, bulimia, asthma,  
 CC Parkinson's disease, acute heart failure, hypertension, hypertension,  
 CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,  
 CC stroke, ulcers, allergies, benign prostatic hyperplasia, migraine,  
 CC psychotic and neurological disorders, autism, multiple sclerosis,  
 CC Alzheimer's disease, and other neurodegenerative diseases, sleep  
 CC disorder, epilepsy, cardiovascular diseases, arteriosclerosis,  
 CC cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral  
 CC infarction, peripheral vascular disease, Raynaud's disease, kidney  
 CC diseases, gastrointestinal disorders, motility disorders and conditions  
 CC of delayed gastric emptying, post-operative or diabetic gastroparesis,  
 CC diarrhoea, inflammation, chemotherapy induced injury, tumor invasion,  
 CC immune disorders, arthritis, endotoxin shock, sepsis, complications of  
 CC diabetes mellitus, and severe mental retardation and dyskinesias, such  
 CC as Huntington's disease or Gilles de la Tourette's syndrome.

SO Sequence 691 AA;

Query Match 33.4%; Score 1322.5; DB 22; Length 691;

Best Local Similarity 39.5%; Pred. No. 1.4e-104; Matches 281; Conservative 143; Mismatches 251; Indels 37; Gaps 17;

QY 54 CLKPECIEAAMALISVNI SVPCDNFRACDGNISNPIEDMPSYGYVWLRHNVLD 113  
 Db 1 CTPPGCVIAAARILQMDPTTEPCDDFYQACGGLRRHVIPETNSRISIPVLRDELVE 60  
 QY 114 KKELEKSISSRRDTEAIOKAKILYSSCMNEKAKEDKAPLHITHSPFMPVLESN 173  
 Db 61 IKAVLENSTA--KORPAVEKARILYRSCMNQSYTERKGSPLLDIL--EYVGGAQAMDR 117  
 QY 174 IPEBGWMSR---KSLQTLATEPBGQYSNVTIRLYVSPDDKASNHILKDOATLSLA 230  
 Db 118 -----WNETVGLWELETRQALNMSQFNRRVLLDLTMDNDQSSRHIIYDQPLGMP 171  
 QY 231 VREDYLDNSTEAKSYDALYKENVDTAVTL--GANSR---AEHMKSVLRLEIKIAEL 284  
 Db 172 SREYFENGSGNRK--VREYILOPMSVATILREDNLPDSCVLOEDMVOULETQTLA 230  
 QY 285 MIPHNRPSE--AMYNKNIISLSAM--IPOFWLGYIKYIDIRLYPHLK--DISPENYV 340  
 Db 231 TVPOERHDVIALYHRMGLLELOQFGLKGFNMTLFIQYVLS-----VKIKLPPEVY 285  
 QY 341 VRVPQFQDLFRILGSEKRTIANYLVWRYVSRIPMLSRPQYRLDESRYVQGTITLL 400  
 Db 286 YGIPYLONLNLIIDTYSARTIONYLWRLVLDRIQSLSGREFQDTRVNRKALFGTWEE 345  
 QY 401 PQMDKVNFISSALPYVVGKAFVDVYFOEDKKEMMELEYGVGMATIDMLEKENEMDAG 460  
 Db 346 VRMRECVGYVNSNMENAVGSLYVREAFPGDSKMWRELIDKVTAVVEILD--ELGMDEE 404  
 QY 461 TKRAKAKARAVLAKVGYPEFLMNDTH--VNEDLAKIKSEADYFGNVLQTRKTLAOSDF 518  
 Db 405 SKKKAQEKAMSIREDQGHDIYLEEMNRRLDEESNLNFSDDLFEENSLQMLKYGAGR 473  
 QY 519 FWLKRAVPKTEFTPTNPTNAFYSASTNOIRPAGLELOKPFMGTEYPRSLSYGATGV 576  
 Db 465 KRLREKVDPMILWITIGAAVNAFYSPNRNOIYVPAIGILOPPF--SKEQQALNFGSIGAVI 523  
 QY 579 GHEFTHGFDNNGRKDYKNGNDLPMWSTSESEKFEKTKCMINQYSNTYWKAG-LNVK 635  
 Db 524 GHEITHGFDNCRNDRDKNGNMWMSNFSTQHFREOSECMITQYGNYSMDLADQONV 592  
 QY 636 RTLGENDNGGLREAFRAKRWINDRROGLEEPLLPITFTNNQLEFLSYAHRCMS 695  
 Db 584 NTLGENIADNGCVRAQYKAYLKKM--AEGKQDQLPGLDITHTQLEFTINAYQWCS 649  
 QY 698 YRPFARQVOIGAHSPQPRVNGAISNSEFOKAFNCPNSTNMNGMSCLM 749  
 Db 641 YRPFARQVOIGAHSPQPRVNGAISNSEFOKAFNCPNSTNMNGMSCLM 749

Thu May 22 07:48:40 2003

us-09-913-955a-1.rag

Page 15

Search completed: May 21, 2003, 18:47:44  
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Thu May 2 07:48:40 2003

us-09-913-955a-1.ra1

Page 1

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OM protein - protein search, using sw model

Run on: May 21, 2003, 18:46:24 : Search time 30 seconds  
(without alignments)  
734.592 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/1aa/PCITUS\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1257	31.8	703	US-08-646-273-25	Sequence 25, Appl
2	1257	31.8	753	US-08-646-273-36	Sequence 36, Appl
3	1248.5	31.5	758	US-08-289-112-2	Sequence 2, Appl
4	1241.5	31.4	708	US-08-646-273-23	Sequence 23, Appl
5	1241.5	31.4	754	US-08-646-273-30	Sequence 30, Appl
6	1184	29.9	787	US-08-574-763-2	Sequence 2, Appl
7	983.5	24.8	775	US-09-305-640-2	Sequence 2, Appl
8	963.5	24.3	567	US-08-646-273-19	Sequence 19, Appl
9	527.5	13.3	189	US-08-646-273-14	Sequence 14, Appl
10	246	6.2	181	US-09-305-640-4	Sequence 4, Appl
11	116	2.9	725	US-08-813-940-25	Sequence 25, Appl
12	114.5	2.9	990	US-08-393-625-20	Sequence 20, Appl
13	114.5	2.9	990	US-08-466-961A-20	Sequence 20, Appl
14	114.5	2.9	990	US-08-645-193B-15	Sequence 15, Appl
15	108	2.7	681	US-08-655-345-4	Sequence 4, Appl
16	108	2.7	681	US-09-183-275-4	Sequence 4, Appl
17	108	2.7	681	US-09-183-275-4	Sequence 4, Appl
18	108	2.7	681	US-09-183-275-4	Sequence 4, Appl
19	108	2.7	681	US-09-183-275-4	Sequence 4, Appl
20	108	2.7	681	US-09-183-275-4	Sequence 4, Appl
21	108	2.7	681	US-09-183-275-4	Sequence 4, Appl
22	108	2.7	681	US-09-183-275-4	Sequence 4, Appl
23	108	2.7	681	US-09-183-275-4	Sequence 4, Appl
24	108	2.7	681	US-09-183-275-4	Sequence 4, Appl
25	106.5	2.7	803	US-08-062-368-2	Sequence 2, Appl
26	105.5	2.7	548	US-09-601-091-2	Sequence 2, Appl
27	105	2.7	479	US-08-484-106-10	Sequence 10, Appl

28	105	2.7	479	US-08-484-106-10	Sequence 10, Appl
29	103.5	2.6	548	US-09-601-091-4	Sequence 4, Appl
30	103.5	2.6	548	US-09-398-395A-52	Sequence 52, Appl
31	103.5	2.6	878	US-09-255-829-12	Sequence 12, Appl
32	103.5	2.6	907	US-09-255-829-16	Sequence 16, Appl
33	103.5	2.6	953	US-09-255-829-14	Sequence 14, Appl
34	103.5	2.6	1013	US-09-255-829-18	Sequence 18, Appl
35	103	2.6	871	US-09-255-829-2	Sequence 2, Appl
36	103	2.6	871	US-09-255-829-8	Sequence 8, Appl
37	103	2.6	871	US-09-255-829-26	Sequence 26, Appl
38	103	2.6	873	US-09-255-829-6	Sequence 6, Appl
39	103	2.6	894	US-09-255-829-4	Sequence 4, Appl
40	103	2.6	1296	US-08-480-604A-28	Sequence 28, Appl
41	103	2.6	1296	US-08-405-496A-28	Sequence 28, Appl
42	103	2.6	1296	US-08-915-136-28	Sequence 28, Appl
43	103	2.6	1296	US-08-286-819A-29	Sequence 29, Appl
44	103	2.6	2291	US-08-980-357-29	Sequence 29, Appl
45	101.5	2.6	607	US-09-134-001C-2994	Sequence 2994, Ap

#### ALIGNMENTS

RESULT 1  
US-08-646-273-25  
Sequence 25, Application US/08646273  
Patent No. 6066502  
GENERAL INFORMATION:  
APPLICANT: Krieger, Burkhard, Seuburger, Harald, Meyer, Thomas, Schmidt, Heino  
APPLICANT: Martini, Jacob, Elard, Olier, Rainer, Subkowski, Thomas, Hillen, Heino  
TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESS: Kell & Weinlauf  
STREET: 1101 Connecticut Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
OPERATING SYSTEM: IBM AT-compatible, 80486 processor  
SOFTWARE: WordPerfect version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,273  
FILING DATE: 16-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP94/03706  
FILING DATE: 11-NOV-1994  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 703 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-273-25  
Query Match 31.8%; Score 1257; DB 3; Length 703;  
Best Local Similarity 37.6%; Pred. No 5, 6e-115;  
Matches 281; Conservative 126; Mismatches 276; Indels 64; Gaps 21;  
OY 21 IALVFVGGTLVLTITFLVSGQLISLQAKQCEYCLKECEIAAAILSKYNLSVPCDNF 80  
DB 3 VIVIVL-----LAAGVACIALALGIQYCRSPSVLSACVSVSSILSSMDPTVDPCHDF 58  
OY 81 FRPACDGISNNPPEDEMPISGVYVWLRHNVDLKELEKISRRRDEAIOKAKIYS 140  
DB 59 FSYAGGIRKANPVPDGHSGRTSINLMEHQAIKILLENSTA--SYSEKRAQYIYR 116  
OY 141 SCMNEKALEKADARILHLRHSFPMFVLESNIGPEGVSEKRSILQTLATFRGOYSN 200

```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 753 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-646-273-36

Query Match      31.8%, Score 1257, DB 3, Length 753;
Best Local Similarity 37.6%, Pred. No. 6,3e-115;
Matches 281; Conservative 126; Mismatches 276; Indels 64; Gaps 21;

Db 117 ACNMETRIEELRAKPLMELIERLG-GWNI-----TGPAKDNFQ--DTLOVTAHYRT 166
Qy 201 SVFIRLYVSPDDKASNEHILKLDQATLSIAVREDYLDNSTEAKSYRAALKKEMVDATVLL 260
Db 167 SPFFSVYVYADSKNSNSNVIOVDOSGLGSPRDYLL-NKTENEKLVLTGYLNTVQGLKLL 225
Qy 261 GANSRA-EHDMKSVLRLEIKIAEIMIPHENRTSEAM-YKMNISLSAMIPOFDMGYI 318
Db 226 GGGDEEAIROPQOQILDFETALANITIPQEKRRDEELIHKVYAAELQTLAPAINLPF- 284
Qy 319 KKVIDTLRYPLKDISPENNVVVRPOYFKDLPRILGSEKKTITANTLVARMYSTRPML 378
Db 285 ---LNTIFYP--VEINSEPIVYDKLEYLQISTLTINTDRCLLNNMIMNLVTKTSSEFL 339
Qy 379 SRRQYRMLESRYIOGT-TTLRPQMDKCVNFESALPYVVGKMFVDVYFOEDKKEEMEE 437
Db 340 DQRFQDADEKFMWYGTCKTKCLPRMKFCVSDENNLGALGPMFKATFAEDSKSIATB 399
Qy 438 LVEGVRAFTDMLKEKEMMDAGTKRKAKEKAAVLAQVYEPFIM-----NDTHV 488
Db 400 ILEIKAFEEEL-STLKMDDEETRSKAKADAIYIMIGYPMFINDPKELDKVFNDYTA 458
Qy 489 NEDLKAIFSEADYFGNVLTQTRKYLAOSDFEW-----LRKAVKTEMTPTPTVAEFS 542
Db 459 VPDL-----YFENAMRF-----FNSMRYVTADQLRKANRQMSMTPTPMVAAYIS 503
Qy 543 ASTNOIRFPAGELQKPPFMTETPRSLSYGALGIVGHEFTGFDNNGKRYDKNGLDWP 602
Db 504 PTNKEIVFPAGILQAPFYTRSS-PKALNFGGIGVVGHELTHTAFDOGREYDKDGLRPM 562
Qy 603 WTESEKEFEKTKCMINQSYNYMKAGLNYGKRTGENTADNGLEAREARAKWTN 662
Db 563 WKNSVYEAERQTECHVEQYSN--SYNGEPVNGRHTLENTADNGLEAARAYQNW- 619
Qy 663 DRQGLEEPLPGITFTNNQLEFLSYAHVRCNSYREARQVOIGASHPPQRYNGAIS 722
Db 620 --KNGAEHS-LPTLGLTNQLEFLGFAQWCSVRTPESHGELLIDPHSPSFRYIGSL 677
Qy 723 NSEEFQAFNCPNSTMNNGMDSCLRM 749
Db 678 NSKEFSEHRCPPGSPMN-PRHKEVW 703

RESULT 2
US-08-646-273-36
; Sequence 36, Application US/08646273
; Patent No. 6065502
;
; GENERAL INFORMATION:
; APPLICANT: Kroege, Burkhard, Seuburger, Harald, Meyer, Thomas, Schmidt,
; APPLICANT: Martin, Jacob, Elard, Oter, Rainer, Subowski, Thomas, Hilten, Heinz.
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: Kell & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; OPERATING SYSTEM: IBM AT-compatible, 80486 processor
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646, 273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 36:

```

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 753 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-646-273-36

Query Match      31.8%, Score 1257, DB 3, Length 753;
Best Local Similarity 37.6%, Pred. No. 6,3e-115;
Matches 281; Conservative 126; Mismatches 276; Indels 64; Gaps 21;

Qy 21 IALVYFGGTVLGLTFLYSGGLSLQAKQECIAKPCICIAAAIISKVLSPDCDF 80
Db 53 VLVVL-----LAAGVACLAAGIQYRRSPSCVSEACVSTSLISSMDPYDPCDF 108
Qy 81 FEPACDGNINNPIDEDMPSGYVPMVLRNVDLKLKELLEISIRRRDTEAIQAKIYS 140
Db 109 FSYACGGWIKANPVDPGSRWGTFSNLWEHNOAIKHLLENSTA--SYSEAKRAQYYR 166
Qy 141 SCMNKATEKADAPLILHNSPPRPVLENSNGPESWSEKFSLLQTLAFRGQYSN 200
Db 167 ACNMETRIEELRAKPLMELIERLG-GWNI-----TGPAKDNFQ--DTLOVTAHYRT 216
Qy 201 SVFIRLYVSPDDKASNEHILKLDQATLSIAVREDYLDNSTEAKSYRAALKKEMVDATVLL 260
Db 217 SPFFSVYVYADSKNSNSNVIOVDOSGLGSPRDYLL-NKTENEKLVLTGYLNTVQGLKLL 275
Qy 261 GANSRA-EHDMKSVLRLEIKIAEIMIPHENRTSEAM-YKMNISLSAMIPOFDMGYI 318
Db 276 GGGDEEAIROPQOQILDFETALANITIPQEKRRDEELIHKVYAAELQTLAPAINLPF- 334
Qy 319 KKVIDTLRYPLKDISPENNVVVRPOYFKDLPRILGSEKKTITANTLVARMYSTRPML 378
Db 335 ---LNTIFYP--VEINSEPIVYDKLEYLQISTLTINTDRCLLNNMIMNLVTKTSSEFL 389
Qy 379 SRRQYRMLESRYIOGT-TTLRPQMDKCVNFESALPYVVGKMFVDVYFOEDKKEEMEE 437
Db 390 DQRFQDADEKFMWYGTCKTKCLPRMKFCVSDENNLGALGPMFKATFAEDSKSIATB 449
Qy 438 LVEGVRAFTDMLKEKEMMDAGTKRKAKEKAAVLAQVYEPFIM-----NDTHV 488
Db 450 ILEIKAFEEEL-STLKMDDEETRSKAKADAIYIMIGYPMFINDPKELDKVFNDYTA 508
Qy 489 NEDLKAIFSEADYFGNVLTQTRKYLAOSDFEW-----LRKAVKTEMTPTPTVAEFS 542
Db 509 VPDL-----YFENAMRF-----FNSMRYVTADQLRKANRQMSMTPTPMVAAYIS 553
Qy 543 ASTNOIRFPAGELQKPPFMTETPRSLSYGALGIVGHEFTGFDNNGKRYDKNGLDWP 602
Db 554 PTNKEIVFPAGILQAPFYTRSS-PKALNFGGIGVVGHELTHTAFDOGREYDKDGLRPM 612
Qy 603 WTESEKEFEKTKCMINQSYNYMKAGLNYGKRTGENTADNGLEAREARAKWTN 662
Db 613 WKNSVYEAERQTECHVEQYSN--SYNGEPVNGRHTLENTADNGLEAARAYQNW- 669
Qy 663 DRQGLEEPLPGITFTNNQLEFLSYAHVRCNSYREARQVOIGASHPPQRYNGAIS 722
Db 670 --KNGAEHS-LPTLGLTNQLEFLGFAQWCSVRTPESHGELLIDPHSPSFRYIGSL 727
Qy 723 NSEEFQAFNCPNSTMNNGMDSCLRM 749
Db 728 NSKEFSEHRCPPGSPMN-PRHKEVW 753

RESULT 3
US-08-289-112-2
; Sequence 2, Application US/08289112
; Patent No. 5688640
;
; GENERAL INFORMATION:
; APPLICANT: Tanigisawa, Masashi
; TITLE OF INVENTION: Endothelin Converting Enzyme-1: A
; TITLE OF INVENTION: Membrane-Bound Metalloprotease That Catalyzes The
; TITLE OF INVENTION: Proteolytic Activation of Big Endothelin-1

```

NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P. O. Box 4433  
 CITY: Houston  
 STATE: TX  
 COUNTRY: USA  
 ZIP: 77210-4433  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/289,112  
 FILING DATE: 10-APR-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parker, David L.  
 REGISTRATION NUMBER: 32,165  
 REFERENCE/DOCKET NUMBER: US/08/289,112  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 713-787-1400  
 TELEFAX: 713-789-2679  
 TELEX: 79-0924  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 758 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-289-112-2

Query Match 31.5%; Score 1248.5; DB 1; Length 758;  
 Best Local Similarity 37.9%; Pred. No. 4.4e-114;  
 Matches 282; Conservative 121; Mismatches 281; Indels 61; Gaps 21;

23 LVVVGGLVLTGLTFLVSGGLSLQAKQCYCLKEPCIEAAALISKVNSVPCDNFPR 82  
 57 LVVVL-ALLAAALVACLAVLGIOYQTRPSVCLSEGCISVTSLSMDPTVPDQDFTT 115  
 83 PACDQWISNPIEDMPCSYGVFWLRHNVDLKLEKLSISRRDPAIOKAKILYSSC 142  
 116 YACGGMKINPVDGHSRGTFSNLMENQALIKHLENSTA--SVSEAKRAQYVYRAC 173  
 143 MNEKAIKADAKPLHLIRHSFPRVLESNIGPEGVSEKRESLQTLATFRGOYSNV 202  
 174 MNEIRIELKAKPLMELIEKLG-GWNT-----TGPMDKDNFO--DTLQVYVSHYHTSP 223  
 203 FTRLYVSPDOKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFWVDVALLGA 262  
 224 FFSVYVSAADSKNSNVIOVDQSGLGPSRDYLL-NKTENEKVLGYLNTVMOGLKLLGG 282  
 263 NS-SRAEHDMKSVLRLEKIAEIMIPHENRSEAM-YNNKMNISELSAMIPQDWLGYIKK 320  
 283 GAEDTIRPQMOOILDFETALANITTPQEKRRDEELIYHKVAAELQTLAPAINLPF--- 339  
 321 VDTFRYLPLKDISPENNVVAVPOYFKDLPRILGSEKRTIANLVLRMYRSRPNRSR 380  
 340 -LNTLFYF--VEINSEPTVIYDKETLSKVSSTLINSKCLNNMTMINVLKRTKISSFLDQ 396  
 381 RFQYRMLESRYLQGT-TTLTPQMDKCVNFIESALPYVVGKAFVDVYQEDKKEMMEELV 439  
 397 RFQDADKEFMEVYGTCKTCLPRKFCVSDENTLGFALGPWFYKATFAEDSKNIASTLI 456  
 440 EGVRAAFIDMLEKEMNDAGTKRKAKEKARAVLAKVGYPEFIM-----NDTHVNE 490  
 457 LEIKAFESTL-STLKWDEDETRKSAKEKADAIYNNIYPNFIMDKELDKYFNDYTAVP 515  
 491 DTKALKEADYFGNVLTQTKYLAQSDFFW-----LKRVPKPTWFTNPTTVNAFVAS 544  
 516 DL-----YFENAMF-----FNFSWRYTADQLKRAKPRDQMSKTPPVNNAIYSP 560

545 TNQIRPAGELQKPFWGTERTPSLSYGAIGVYHBEFTGFDNNGRKYDKNGNDPMWS 604  
 561 KNEIVFAGILQAPFYTRSS-PNALNFGGIGVYVGHLLTAFFDQGEYKDKGNLPRWK 619  
 605 TESEKREKTKCMINQISNYWKRAVLNKGKRTIGENIADNGGLREAFRAYRKWINDR 664  
 620 NSSVEAFKQOTACAVEQYGN--SVNGEPVNGRHTLTGENIADNGGLKAAVRAVQNNV--K 675  
 665 RQGLEPRLPITITNNQPLFLSAHYRCHNSYRREARQVOGANSPPQFRNGAISNS 724  
 676 KNGAEQ-TLPTGLJTNQPLFLSFGYQVCSVRPESSHEGLITDPHSPRFRVIGSISNS 734  
 725 EEPQAFNCPNSYNNRGMDCRLM 749  
 735 KEFSEHCHPPGSPMN-PHEKCEVW 758

RESULT 4  
 US-08-646-273-23  
 Sequence 23, Application US/08646273  
 Patent No. 6065502  
 GENERAL INFORMATION:  
 APPLICANT: Kroeger, Burkhard, Seubberger, Harald, Meyer, Thomas, Schmidt,  
 APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hilten, Hein  
 TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Keil & Weinkauf  
 STREET: 1101 Connecticut Avenue  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
 COMPUTER: IBM AT-compatible, 80486 processor  
 OPERATING SYSTEM: MS-DOS version 6.0  
 SOFTWARE: WordPerfect version 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,273  
 FILING DATE: 16-NOV-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION NUMBER:  
 APPLICATION NUMBER: PCT/EP94/03706  
 FILING DATE: 11-NOV-1994  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 708 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-646-273-23

Query Match 31.4%; Score 1241.5; DB 3; Length 708;  
 Best Local Similarity 37.9%; Pred. No. 1.9e-113;  
 Matches 282; Conservative 120; Mismatches 282; Indels 61; Gaps 21;

23 LVVVGGLVLTGLTFLVSGGLSLQAKQCYCLKEPCIEAAALISKVNSVPCDNFPR 82  
 7 LVVVL-ALLAAALVACLAVLGIOYQTRPSVCLSEACTSVTSLSMDPTVPDQDFTT 65  
 83 PACDQWISNPIEDMPCSYGVFWLRHNVDLKLEKLSISRRDPAIOKAKILYSSC 142  
 66 YACGGMKINPVDGHSRGTFSNLMENQALIKHLENSTA--SVSEAKRAQYVYRAC 123  
 143 MNEKAIKADAKPLHLIRHSFPRVLESNIGPEGVSEKRESLQTLATFRGOYSNV 202  
 124 MNEIRIELKAKPLMELIEKLG-GWNT-----TGPMDKDNFO--DTLQVYVSHYHTSP 173  
 203 FTRLYVSPDOKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFWVDVALLGA 262  
 174 FFSVYVSAADSKNSNVIOVDQSGLGPSRDYLL-NKTENEKVLGYLNTVMOGLKLLGG 232

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Query Match 31.4%; Score 1241.5; DB 3; Length 754;
Best Local Similarity 37.9%; Pred. No. 2.2e-113;
Matches 282; Conservative 120; Mismatches 282; Indels 61; Gaps 21;

QY 23 LVFVGGTVLTGTTITFLVSGGLSLQAKOECEIEAAMAILSKVNLSDPCDNFR 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 LVVLV-ALLAALVAVLAVLGIQYQTRPRPSVCLSEALSVISLSDMDFVPCQDFET 111
QY 83 PACDQWISNNPREDPMBSYGYPMYLRHVNDLKLLEKLSISRRDATALQAKLLYSSC 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 112 YACGGMKANPVPDQSHSRKGTFSNLMENQALIKLLNSTA--SVSAERDDQYRYNAC 169
QY 143 MNEKIEKADAPLHLIRHSPFRVLESNIGPEGVSEKFSLLQTLATFRQYNSV 202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 170 MNETIEELKAKPMLLEIKLG-GNNT-----TGPMKDKNFO--DTLQVYTSYHHSF 219
QY 203 FRLVYSPDDKASNEHILKLDQATLSLAVREDYLDNSTEASRYDALYKFWDAVLGA 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 220 FFSVYVADSKNSNSNVIQVDDSGGLPSRDYLT-NKTENEKVLGGLYINWVQGLKLLGG 278
QY 263 NS-SAEHDMSVLRLEKIAELMIPHENKTSSEAM-YKMANISELSAMIPOEDMIGYTK 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 279 GAEDTRIPMOQOILDFETALANITTPQKRKRDEELIYKRVTAELQTLAPAINMLPFP-- 335
QY 321 VDTFLYHLKIDISPENNVYVPOFYFDLPRILIGSEKKTATYLVWRMYSRIPNLSR 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 336 -LNTFYTP--VEINSEPIVITDKYLSKSTLINSTKCLINNTMINVLKAKTSSFLDQ 392
QY 381 RFOYMWLEFSRYIGT-TTLTPQMDKCVNFIESALPYVVGKMFVDVYPOEDKEMMEBLV 439
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 393 RQDADEKFMFYMGTKTCLPRKMKCYSDFENTLGLGAPMFVATPAEDSKNIASELI 452
QY 440 EGVRAFAFLDMEKEBMDAGCKRKAERKARAVLAKVYPEIYIM-----NDTHNE 490
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 453 LEIKAFSESL-STLKMDDETRKSAKERAADAIYNMISYPMVIMPKELDVFNQDYAVP 511
QY 491 DLKATFEADYFGVNLQTRKYLQSDPEFW-----LRKAVPTEMTNPTVNAFYAS 544
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 512 DL-----YFENAMF-----FNSWRTADQLKARPRQDMSTPRMVNAYEPT 556
QY 545 TNGQIRPAGLOKRPFGWCTEYPRSLSTYALGYVGHFTHGDNNGKRYDKNGNIDPMWS 604
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 557 KNEIYFPPGILQAPRYTSS--PNALNFGIGIVVGHETHLAFDDGREGDXGNLRPMWK 615
QY 605 TSESEKFEKTKCMHNOYSNYYWKKAGLVNKGKPTLGENIADNGSLREAFRAYRKWINDR 664
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 616 NSSVAEFQOQRAHWEQYGN--SYNGEPVNGRHTLGENIADNGSLKAIIRAYQMWV--K 671
QY 665 RGLEDEPLLPGLTITNNOLFELSYAHVNCNSYRPEAREQYOIGAHSPOPRVNGAISNS 724
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 672 KNGARQ-TLPTLGLNNQLFLSFQVWCVSRTPESSHGILTDHSPSRRFVIGSISNS 730
QY 725 EFOKAFNCPPNSTYNRGDCRLM 749
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 731 KEFSEHFHCPPGSPMN-PHHRCEVW 754
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-08-574-763-2
; Sequence 2, Application US/08574763
; Patent No. 5736376
; GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masashi
; TITLE OF INVENTION: RECOMBINANT ENDOTHELIN CONVERTING
; TITLE OF INVENTION: ENZYME-2 AND ITS USE IN ECE INHIBITOR SCREENING
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA

```



QY 658 RKWINDROGLEBELLPGITFTNNOLFSLYAHVRCNSYRPARARQVIGAHSPQRY 717  
 Db 688 KQWV--REHGPBHP-LPRLKTYTHDQJFLTAFAQNMCKIKRSOSIYLVLTDKHADEHYR 744  
 QY 718 NGAISNEEQKAPNCPNPNSTNRGMDSCRLW 749  
 Db 745 LGSVSOFEERGAHFCHPKDPSPMNPA-HKCSVW 775

## RESULT 8

US-08-646-273-19  
 ; Sequence 19, Application US/08646273  
 ; Patent No. 6066502  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kroeger, Burkhard, Seubberger, Harald, Meyer, Thomas, Schmidt,  
 ; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Heinz.  
 ; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
 ; NUMBER OF SEQUENCES: 36  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kell & Weinlauf  
 ; STREET: 1101 Connecticut Avenue  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
 ; COMPUTER: IBM AT-compatible, 80486 processor  
 ; OPERATING SYSTEM: MS-DOS version 6.0  
 ; SOFTWARE: WordPerfect version 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/646,273  
 ; FILING DATE: 16-NOV-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/EP94/03706  
 ; FILING DATE: 11-NOV-1994  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 567 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-646-273-19

Query Match 24.3%; Score 963.5; DB 3; Length 567;  
 Best Local Similarity 37.7%; Fred. No. 3.8e-86;

Matches 226; Conservative 96; Mismatches 216; Indels 61; Gaps 21;

QY 106 WLRHNVDTKLEKLEKISRRRTDTEAOKAKIYSSCMNKAIEKADAPLHLLHSPF 165  
 Db 12 W-EHNOAI-IKHLLENSTA--SVSEARNDQDEYRACMNETRIEELKAKPLMELLEKLG- 66  
 QY 166 RWPVLESNIGPEGVWSERKESLIQTLATFRGQYSNSVFIRLYVSPDDKASNEHILKLDQ 225  
 Db 67 GWNV-----TGPWMDNFQ--DTLOVYTSHTSPFSVYASADSKNSNSNVIOQDS 117  
 QY 226 TLSIAVEDYLDNSTEAKSYRDALYKEMVDVAVLGANS-SRAEHMKVAVLEKIAEI 284  
 Db 118 GLGIPSDYLL-NKTEKEKLYGLYKYNVQOLKGLGGAGEDTIRPOMQILDPEFALANI 176  
 QY 285 MIPHEMFTSAM-YKNMINSLSAMTPOFMDLYIKVYDTRLYPHLKDISSENVAVRV 343  
 Db 177 TLPQEKREDELLYHKYTAELQTLAPAINMLPF-----LNTIFYP--VEINSSEVIYD 230  
 QY 344 POFENDFRILGSEKRTIANYIVMAYVSRIPNLSRRQYRWLEFSRYIOGT--TLLPQ 402  
 Db 231 KETLSKYSTILNSTKCLNNYIMVNLVKTSSPFDORFODADEKFMVYMGTKTKCLPR 290  
 QY 403 WDCVNFISALPYVYVKMFVDVYFQEDKKEKMEELVEGVRAFTDMEKENEMADAGTK 462  
 Db 291 WKFCVSDTEMTLGFALGPRFVFKATFRAEDSKNIASELILEIKAFEEEL-STLKWMEDETR 349

QY 463 RKAKEKARAVLAKVGYEFIM-----NDTHVNEDLKAIKSEADYFGNVLOTFRYL 513  
 Db 350 KSAKEKADAIYNNIGYIPNINMDPKELDKFNRYTAVPDL-----YFENARF----- 396  
 QY 514 AODDFW-----LRKAVKTEMTFTNPTVNAFYSASTNOJIRFAPGELOKPFFGTEYPR 567  
 Db 397 --FNFMSRYTADQLRRKAPNRDQMSMTPPVNAVYSPTKNEIVFPAGILQAFYIRSS-PN 453  
 QY 568 SLISYGAIVYVGHFTHGFDNNGRKYNLDNPKWSTSESEKREKTKKINISYTW 627  
 Db 454 ALNFGSIGVYVGHFTHGFDNNGRKYNLDNPKWSTSESEKREKTKKINISYTW 627  
 QY 628 KKAAGLVKGRKRLGENIADNGGLREAFRAYRWINDRROGLEBELLPGITFTNNOLF 686  
 Db 512 SVNGEVPVNGRHTLGENIADNGGLKAAARYAYQNWV--KKNAGQ-TLPTLGLTNNQLEFL 567

## RESULT 9

US-08-646-273-14  
 ; Sequence 14, Application US/08646273  
 ; Patent No. 6066502  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kroeger, Burkhard, Seubberger, Harald, Meyer, Thomas, Schmidt, Hein  
 ; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Hein  
 ; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
 ; NUMBER OF SEQUENCES: 36  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kell & Weinlauf  
 ; STREET: 1101 Connecticut Avenue  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
 ; COMPUTER: IBM AT-compatible, 80486 processor  
 ; OPERATING SYSTEM: MS-DOS version 6.0  
 ; SOFTWARE: WordPerfect version 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/646,273  
 ; FILING DATE: 16-NOV-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/EP94/03706  
 ; FILING DATE: 11-NOV-1994  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 189 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-646-273-14

Query Match 13.3%; Score 527.5; DB 3; Length 189;  
 Best Local Similarity 51.8%; Fred. No. 6.6e-44;

Matches 101; Conservative 32; Mismatches 55; Indels 7; Gaps 5;

QY 555 LOKPFWGTEYPRSLSYGAIVYVGHFTHGFDNNGRKYNLDNPKWSTSESEKREK 614  
 Db 2 LQAPFYTRSS-PAVALNFGSIGVYVGHFTHGFDNNGRKYNLDNPKWSTSESEKREK 60  
 QY 615 TKCMINQISYTWKKAAGLVKGRKRLGENIADNGGLREAFRAYRWINDRROGLEBELL 674  
 Db 61 TACMVDQYNY--SVNGEVPVNGRHTLGENIADNGGLKAAARYAYQNWV--KKNAGQ-TLP 115  
 QY 675 GITEFTNNOLFSLYAHVRCNSYRPARARQVIGAHSPQRYVNGAISNEEQKAPNCP 734  
 Db 116 TLTGLTNNOLFSLYAHVRCNSYRPARARQVIGAHSPQRYVNGAISNEEQKAPNCP 175  
 QY 735 PNSTANRGMDSCRLW 749  
 Db 176 PGSPMN-PHMKCEVW 189



```

1 APPLICATION NUMBER: US 08/612,271
2 FILING DATE: 07-MAR-1996
3 CLASSIFICATION: 435
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Deluca, Mark
6 REGISTRATION NUMBER: 33,229
7 REFERENCE/DOCKET NUMBER: UPAP-02220
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: 215-568-3100
10 TELEFAX: 215-568-3439
11 INFORMATION FOR SEQ ID NO: 25:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 725 amino acids
14 TYPE: amino acid
15 TOPOLOGY: linear
16 MOLECULE TYPE: protein
17
18 US-08-813-940-25
19
20 Query Match 2.9%; Score 116; DB 2; Length 725;
21 Best Local Similarity 19.5%; Pred. No. 0.029;
22 Matches 139; Conservative 113; Mismatches 242; Indels 218; Gaps 37;

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Query Match: 19.9%; Score 116; DB 2; Length 725;
Match Local Similarity 12.5%; Pred. No. 0.029;
Matches 139; Conservative 113; Mismatches 242; Indels 218; Gaps 37

QY 109 HNWDLKLELLESISRNRDTEAOKALILYSSCMEKAIEKADKPLHLRHSPRMP 168
      || || | : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 HNDKERDYLIRENYER---EVLQD---YSRNFVTKLLDRAVAK-----KRRFP 111
QY 169 VLESNIPEGWSEKRFSLLOTLATPRGQ-----YNSVPLRLYSPDDKASNEHLKL 222
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 112 TELGAF-----KYYYSYTLKTFDGKRYIEREDRVMAWALLAGDATALIELIV-- 160
QY 223 DQATLSLAVREDYLDNSTEAKSYRADLYKFWDVTFVLLGA--NSSRAEHDMKSVLREIKI 281
      : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 161 -----DELIDG-----RFGQATPFLNSGKKQGEVSGFELLRVEDNM 198
QY 282 AELMIPENRNTSEAMNKNISLMSLMDPQWMLGYIKKVIDTLRYLP---LKOIJSSEN 338
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 199 ESI-----GSSINSLAOLSKRGGV-----ALLTLNREHGAIKENIQSS 240
QY 339 VYVAVPQYFDLFLT--LGSEKRTIANYL-----WBRWYSRIPMLSRPFYRWLEF 389
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 GVIPMKLEAPSYANQLGA--RQGGAVYLLAHHPDIYRFLDTRYENADKIKIKITLSL 299
QY 390 SRVIOGTTTLLPQWDCVNFIESALPYYVVGKMFVDYFQEDKKEMEELVSGVWAPIDM 449
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 300 GVVIPDITFELAKNDOMYLF--PYDV-----BRVYGVFPADISV 338
QY 450 LEKENEMDACKTKKAKERK---AVLAKV-----GYPERIMND-----TH--- 487
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 339 TEKYEWYWDARIKRTIKAREFFQTLAEIGFESGYPYIMFEDTVNRANPIDGKITHSNL 398
QY 488 -----VNEDKAIKFSEADYFGNV--LQTRKYLAOSDF-----FWLR----- 522
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 399 CSEILOVSTPSELFMEDLSYAKVGK--DISCHUGSLINAKIMSDPDRQOILEVAIRALTVR 457
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 523 -----KAVPKTEWFTNPJTVAIFYSASTNOIRPAGELQKPEFWGTE-----YPSRL 569
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 458 HQTHIKSVPSIEQNNDS-----HAIGLOMNHGLIARERIRFYSGSDGIDFTNIYFTYV 512
QY 570 SYGAIGV---IVGHEFTH--GFNDNGKRYKXKNNDLPMWSTSEKKEKRTKCMNOVSN 624
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 513 LYHALRASNRILAERGHFKGPFERS--KVASGEFFKY---TDQIWEKTOYKAOQLPAD 566
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 625 YWVKAGLNVGKRTLIGENIADNGGLREAFARVAKKMINDRQGLLEBPLPGITFNNOJLF 684
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 567 -----AGIRIFTQ-----DDMRRLKESVQAH-----GIYQNOLOAVPFGS--- 602
QY 685 FLSYAVHVCNSYRPEAREVY---QIG-AHSPQORVNGAISNSSEFPKAF 731
      | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 603 -ISYINHSTSIHPYSVKEVYRKGIKGRVYYPAPMTN--DNLEYYEDAY 650

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Thu May 22 07:48:40 2003

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[illegible]

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Db 305 -----IDFYIDYSRNEMLQSLADNISEAAYIIMLSPEH-----GTKTR----- 345
QY 471 AVIATKGYPEFLMNDTHVNEDLKAIK--FSEADYFGVLOTOKRYLAOSDEFFWLK-----A 524
Db 346 -----NHEFFM--DKYGEFODLVNKKOLLSINFSG--YPKKDSYSFGNNNAFLKEKYL 397
QY 525 VKPTEW--FTNPNTYNAVYSASTNOIRPPAG--ELOKRPFPMWETPRSLSGAIGVGH 561
Db 398 IONNHSIETEDVDNKLKNNTVYSKINAPVSTELYSLETIFGNSIKGDEPAVISPLIGS- 456
QY 582 FTHGCDNNKRYDK--NGULDFPMWSTSESEKREKTKCMINOYSNY-----YKKAG 631
Db 457 -----FNGATFGRPTGNF-----NIKKNOLOKEIVHHYNNMENDLEISQLEAP 504
QY 632 LNVKCRKRLGENDNGCLREAFRAYKRWINDROGLEEP-----LLPGTTFNNOL 683
Db 505 LNSRNVNLLNN-----RIYTCLN-----LNLKPSDIDINDIFGATF--NKL 546
QY 684 FFLSYAH 690
Db 547 YLYSEKH 553

RESULT 13
US-08-466-961A-20
/ Sequence 20, Application US/08466961A
/ Patent No. 5843709
/ GENERAL INFORMATION:
/ APPLICANT: Entlan, Karl-Dieter
/ APPLICANT: Gtz, Friedrich
/ APPLICANT: Schnell, No. 5843709bert
/ APPLICANT: Augustin, Johannes
/ APPLICANT: Engelke, Gernar
/ APPLICANT: Rosenstein, Ralf
/ APPLICANT: Kaletta, Cortina
/ APPLICANT: Klein, Cora
/ APPLICANT: Wieland, Bernd
/ APPLICANT: Kupke, Thomas
/ APPLICANT: Jung, G. nher
/ APPLICANT: Kellner, Roland
/ TITLE OF INVENTION: Biosynthetic Process for the preparation of
/ TITLE OF INVENTION: Chemical Compounds
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox
/ STREET: 1100 New York Avenue, NW
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,961A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/392,625
/ FILING DATE: 22-FEB-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/876,791
/ FILING DATE: 30-APR-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/784,234
/ FILING DATE: 31-OCT-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Esmond, Robert W.
/ REGISTRATION NUMBER: 32,893
/ REFERENCE/DOCKET NUMBER: 0652, 0980004
/ TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 990 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-466-961A-20

Query Match 2.9% Score 114.5; DB 2; Length 990;  
 Best Local Similarity 19.6%; Pred. No. 0.07; Indels 149; Gaps 30;

Matches 107; Conservative 92; Mismatches 199; Indels 149; Gaps 30;

QY 196 GQYSNSVFIRLYSPDDKASNEHIILKDAQATLSLAVREYLDNSTEAKSYRDAL-----Y 250  
 DB 104 GEFSENNIKI-----KDSFHKDKVKGIDGMVLYKHV-YLE--SDYTYKDSFVIMNQ 155  
 QY 251 KFMVDVAVLLGANSRAEHDMKSVLRLEIKTAELIMPHENRTSEAMYNK-----300  
 DB 156 NYIYNRRLYLDNNSSTIEKRNVDLSVKYNSILVFI-HENSKKNITYEELVOLISSKYSI 214  
 QY 301 -NISELSAMIPQDFMLGYIKKYIDRLYPHLKDISENVVAVVQYKDFRILIGSERK 359  
 DB 215 ENKEEYKVFQEL-----INKEIIFSDLRPTLENKNP-----IDYIINSLNP 256  
 QY 360 KTIANYLVWAV-----YSRIPNLSRRFOYRWLEFSRVIGTTLPLPQWDKCVNFIE 411  
 DB 257 K--NSLVGTLLINISNEITKYSKMP--LGKGEYKLYDI-----VNLMSQLFVSKNYIQ 304  
 QY 412 SALPYVVGKMFVDYVFOEDKKEEMELVEGV-RWAFIDMLEKENMDAGTKRKAKEKAR 470  
 DB 305 -----IDYIIDSRLNELKOSLADNISEAVIIMLSPNHF---GTKTIR-----345  
 QY 471 AVLAQVGYPEFIMNDTHVNDLKAIR--FSEADYFGNVLOTRKYLAOSDFEMLRK-----A 524  
 DB 346 -----NYHEFEF-DKYGFEQVLNKLQSLDINGFC-YPKKDSYSFSNNIAFLKEKYTLA 397  
 QY 525 VKPTW--FTNPTVNAFYSASTNOIRPAG-ELQKPFWGTETPRSLSYGAGIVVGE 581  
 DB 398 IONNSHIEITENDVKNLEKNNTVSKINAPVSTIEYSEIYFNGSIKGYEDFVISPILGS- 456  
 QY 582 FTGFGDNNGRKYYK-NGNLDPMWSTSESEKREKTKCMINOISNY-----YMKAG 631  
 DB 457 -----FNAGATFGRPTGNF-----NKKKNQLOKEIYVHHYNNVNNENDELSQLEAP 504  
 QY 632 LNVKGRITLGENIADNGGLREAFRAYRKWINDRQGLEEP-----LLPGITFTNNOL 683  
 DB 505 LNSRNVNILLNN-----RIYNTCLN-----LNPKSDIDINDIFIGATF--NKL 546  
 QY 684 FFLSYAH 690  
 DB 547 YLYSEKH 553

RESULT 14

US-08-645-193B-15

Sequence 15, Application US/08645193B

Patent No. 5962253

GENERAL INFORMATION:

APPLICANT: Kupke, Thomas

APPLICANT: Goltz, Friedrich

APPLICANT: Kempfer, Christoph

APPLICANT: Jung, Gunther

TITLE OF INVENTION: Oxidative Decarboxylation of Peptides

TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/645,193B  
 FILING DATE: 13-MAY-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Esmond, Robert W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 0652,1540000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 990 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: protein  
 US-08-645-193B-15

Query Match 2.9% Score 114.5; DB 2; Length 990;  
 Best Local Similarity 19.6%; Pred. No. 0.07; Indels 149; Gaps 30;  
 Matches 107; Conservative 91; Mismatches 200; Indels 149; Gaps 30;

QY 196 GQYSNSVFIRLYSPDDKASNEHIILKDAQATLSLAVREYLDNSTEAKSYRDAL-----Y 250  
 DB 104 GEFSENNIKI-----KDSFHKDKVKGIDGMVLYKHV-YLE--SDYTYKDSFVIMNQ 155  
 QY 251 KFMVDVAVLLGANSRAEHDMKSVLRLEIKTAELIMPHENRTSEAMYNK-----300  
 DB 156 NYIYNRRLYLDNNSSTIEKRNVDLSVKYNSILVFI-HENSKKNITYEELVOLISSKYSI 214  
 QY 301 -NISELSAMIPQDFMLGYIKKYIDRLYPHLKDISENVVAVVQYKDFRILIGSERK 359  
 DB 215 ENKEEYKVFQEL-----INKEIIFSDLRPTLENKNP-----IDYIINSLNP 256  
 QY 360 KTIANYLVWAV-----YSRIPNLSRRFOYRWLEFSRVIGTTLPLPQWDKCVNFIE 411  
 DB 257 K--NSLVGTLLINISNEITKYSKMP--LGKGEYKLYDI-----VNLMSQLFVSKNYIQ 304  
 QY 412 SALPYVVGKMFVDYVFOEDKKEEMELVEGV-RWAFIDMLEKENMDAGTKRKAKEKAR 470  
 DB 305 -----IDYIIDSRLNELKOSLADNISEAVIIMLSPNHF---GTKTIR-----345  
 QY 471 AVLAQVGYPEFIMNDTHVNDLKAIR--FSEADYFGNVLOTRKYLAOSDFEMLRK-----A 524  
 DB 346 -----NYHEFEF-DKYGFEQVLNKLQSLDINGFC-YPKKDSYSFSNNIAFLKEKYTLA 397  
 QY 525 VKPTW--FTNPTVNAFYSASTNOIRPAG-ELQKPFWGTETPRSLSYGAGIVVGE 581  
 DB 398 IONNSHIEITENDVKNLEKNNTVSKINAPVSTIEYSEIYFNGSIKGYEDFVISPILGS- 456  
 QY 582 FTGFGDNNGRKYYK-NGNLDPMWSTSESEKREKTKCMINOISNY-----YMKAG 631  
 DB 457 -----FNAGATFGRPTGNF-----NKKKNQLOKEIYVHHYNNVNNENDELSQLEAP 504  
 QY 632 LNVKGRITLGENIADNGGLREAFRAYRKWINDRQGLEEP-----LLPGITFTNNOL 683  
 DB 505 LNSRNVNILLNN-----RIYNTCLN-----LNPKSDIDINDIFIGATF--NKL 546  
 QY 684 FFLSYAH 690  
 DB 547 YLYSEKH 553

RESULT 15

US-08-655-345-4

Sequence 4, Application US/08655345

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Patent No. 5830742
GENERAL INFORMATION:
APPLICANT: Black, Roy A.
APPLICANT: Rauch, Charles
APPLICANT: March, Carl J.
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: TNF- $\alpha$  CONVERTING ENZYME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.2
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,345
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,614
FILING DATE: 20-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,458
FILING DATE: 8-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2507-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-345-4

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Query Match 2.7%; Score 108; DB 2; Length 681;  
 Best Local Similarity 18.9%; Pred. No. 0.16; Indels 266; Gaps 38;  
 Matches 140; Conservative 96; Mismatches 237;

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QY 93 PIPEDMPGVYVWLRHNVDLKLEKLSISRRDTEALQAKILYSSCMNEKAIEKAD 152
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 1 PRPPDPGFGPH-----QRLEKLDLSLDYD-----ILSLNIOGHSVRKRD 42
QY 153 AKPLIHT--LRHSFRRPVLESNIGPGVSEKRFSLQTLATFRGOYSNSVFIRLYVS 209
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 43 LQTSFHVETLLTFSLAK-----RHFKLYLTSSTERESQNFV-----VV 81
QY 210 PDDKASNHILKLDQATISLAVREDYLDNSTEAKSYRDALKKFWADAVILIGANSRAEH 269
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 82 VDGKNESEYTKWODEFTGHVGEPP--DSRYLA-----HIRDDVITIRINTDGAHY 130
QY 270 DMKSVLRLEIKLAEIMIPHENTSE--AMYNKNNISLSAM--IPOEDMLGIYIKKVIDTR 325
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 131 NIEPLMR-----VNDTKKRLMLYKSEDIKNVSRLOSPKV--CGYLKVDNEL 177
QY 326 LYPHUKDISPSENVVYV-----POYFD-----LFRILGSEKRTIANYLYVR 369
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 178 LPKGLVDEPEPELVRHRADPDMKNCKLLVADHRYRYMGREGSESTTNLYL-- 235
QY 370 MYSTRIPNLSRRFOYRW-----LEFSRVIOGTTLLPQWDKCVNFIESALPYV 418
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 236 ELIDRVDDIYRNTS--WDNAGFKYGIQIEQIRILKSPQEVKP--GEKHYNMAKS----- 286

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QY 419 GKMFVYVQEDK-----KEMMEELVEGVRAFLDMLEKENEMWDAGTKRRAKARAVL 473
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 287 -----IPNEEKDAMDVKMLLEQSFDI-----AEEASRYCL 317
QY 474 ARV-GYPEFIMNDTHVNEDLKAIKFSADYRGVNLQTKRYLAQSDFWLRAVKTETFT 532
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 318 AHLEFYQDFDMGTL-----GLAVYGSPPRANSHGV-----CRK----- 350
QY 533 NPTVNAFYSASTNLRPAGELOKPFMGTEPRSLSYG-----AIGVIHGEFTHGF 586
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 351 -----ATIS-----PVG--KKNTILNSGLISTKNYKGTILTKENDLYTTHLGHN 394
QY 587 DNNGRKYDKNGNIDPWWSTSESEKREKTKCMINQYSNYWKAGLVNK----- 636
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 395 ---GAHDPDG-----LAECAPNEDQGGKVMYPYIAVGDHNNKMFNSN 435
QY 637 --KRITGENIADNGILREAF--AYRKINDRQGLEFFLPGIIFTNQLEFLSAHYRC 693
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 436 CSKOSIYKTIESKA--QECFOERSNKCVCNSVHDEGECDPQIMYLNND-----TCC 485
QY 694 NSYRPEAREVOYQIHAHSP-----QFRVNGAISNSEEFOKAFN-----C 733
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 486 NS--DCTLKEGYQCSDRNSPCKCKNOFE-----TAQKCGEALINATCKGVCYIGNSSEC 538
QY 734 PP-----NSTMNRGMDSCR 747
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 539 PPQNAEDDTVCLDLGCK 557

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Search completed: May 21, 2003, 18:50:38  
 Job time : 34 secs



Db 248 IIVIDPFLGMPREXYENGSGNRK-VREAYLOFMVSVATILREDANLPDSCLOVEDMY 306  
Qy 273 SVLRLEIKIAIMIPHENTSE-AMYNKMISELISAM-IPQDMGLYIKVYDTRLYPH 329  
Db 307 QVLELEQLKAYVPOEERHDVATLHRMGLLEQSOFGKGNWFLFQTVLSS----- 361  
Qy 330 LK-DISPESENVYVPOYFDLFRILGSEKKTIANLVWVWYSRIPNLSRFRQWLE 388  
Db 362 VKILDEDEVVYGIPIQLNLENIIDTYSARTIONTLVRLVLDRLGSLQSFKOTRYN 421  
Qy 389 FSRVIOQTLLPQMDKCVFISALPYVYGMFVDYFOEDKEMMEELVGSVRAFLD 448  
Db 422 YRRLFTETVYEVWRKCVGVYVSNMENAVALGSLYVEAFPGDSKSMVRELIDKRVFVE 481  
Qy 449 MLEKENMDAGTRKRAKRAVLAQVGYPEFIMNDTH--VVEDLKAIKESADDFGV 506  
Db 482 TLD-ELGMDDESKKRAQKQEAAMIRQDIGHPTILEMNRDDEEYSNLFSDLTFEYS 540  
Qy 507 LQTRKYLQSDFFWMLKRAVKTETMTNPTVNAFYASSTNQLRFPAGELOKPFMGTEYP 566  
Db 541 LQMLKVAQASLRKRLREKVDPLMIIIGAAYNAFYSPNNQIYFPAIGLIQPPFF-SKEGP 599  
Qy 567 RSLSYGAGIYVHEFTHGDNNGRYDKNLDPMWSTSESEKREKTKMINTSYNTY 626  
Db 600 QALNFGIGVYGHETHTGDDGNFDRKNGNMDSNFSSTQHFREOSECMYIOGANS 659  
Qy 627 WKRAQ-LNVKGRRLTGLNADNGLEAFRAVRYKWINDRROGLEBLLGITFNNQLPF 685  
Db 660 WDLADQNVNGFMTLEGNLADNGVQAQKAYIKM--AEGKDDQLGDLTLHQLEPF 716  
Qy 686 LSAHRCMSYRPEARBOYQGAHSPPOFRVNGAISNSEEFOKAFNCPNSTMNGMS 745  
Db 717 INAQWCSYREFAIQSIKTDVHSLPKRYVLSLQNLAAFDHFCARGPMH-PKER 775  
Qy 746 CRLM 749  
Db 776 CRYW 779

RESULT 2  
US-09-978-295A-526  
Sequence 526, Application US/0978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
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APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366

PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 30.9%; Score 1223; DB 9; Length 736;  
Best Local Similarity 35.2%; Pred. No. 3e-91;

Matches 267; Conservative 145; Mismatches 307; Indels 40; Gaps 18;

QY 2 EAETGSSV--ETGKANGPFIAL-VYFVGTVLGIIF--LYSGL-LSLAKDEYCL 55  
DB 7 ELGAGSNVGFQKGTROLLGSRTOLEVLVAGSLALLGLGCVALGVYHRDPSSHSTCL 66  
QY 56 KPCIEAAMALISKVNLVDPDCDNFFRACDGNISNNPIEDMPSGVYPMLRHNVDLKL 115  
DB 67 TEACIRVAGKILLESIDRGVSPCEDFYOFSCGWRIRRPDLGDSRKNFTFSLMDQAIL 126  
QY 116 KELLEKSIRKRDTEALQAKILYSSCMNEKALEKADAKPLHLIRHSPRPWLESNIG 175  
DB 127 KHLLENT-TENSSSEAAQKQREFLSLOVERIEELGACPLRLDI-----EKIG 174  
QY 176 P---EGWSEKKEFSLQTLATFRGOYSNVETIRLYVSPDDKASNEHLIKDQATLSLAR 232  
DB 175 GWNITGPDODNF--MEVLAIVAGTYRATFTFTVYISADSKSSNSNVIOVDOSGLFPSR 232  
QY 233 EDVLDNSTEAKSYRDALYKPMVDJAVLLGANSRAEHDMKSVLRLEIKIAEIMPH-ENR 291  
DB 233 DYYL-NRTANEKYLTAVIDYMEELGMLGRPSTREQMOQVLELEIQALNTIVPODDOR 291  
QY 292 TSEAMYNKANISELAMIPFDMLGIYIKKYIDRLRPLHLKDIPSSNVVVVVPQFFKDLF 351  
DB 292 DEEYIHKMSISBLQALAPMDMLEFLSLSP-----LELSDSEPVVVYVGMDYLOQVS 345  
QY 352 RIIGSEKRTIANYLWVRWYSRIPNLISRRFOVRWLEFSRVIGCT-TITLLPQMDCVNFI 410  
DB 346 ELINRTEPSILNNYILWNLVQKTTSSLDREFESAQEKLLLETLYGKICKSVPMQTCISNT 405



QY 411 ESALPYVGMKMFVYFOEDKEMMEELVEGVMAFIDMLEKENEMWADGTRKAKERAR 470  
 Db 406 DDLGFGALGSLFKATFDROSKETIAEGMISEIRAFEEEL-GOLVWMDKTRQAARERAD 464  
 QY 471 AVIAKGYEELTMDTHVEDLKAIFSEADYFGVNLQTRKYLAOSDFEFLRAVPTKEM 530  
 Db 465 AIYDMIGFDFLEPKELDDYDGEISEDSFQNMNLNYSAKVMADQLRPPSRDOW 524  
 QY 531 FTNPDTNAYFASSTNOIREPAGELQKPFWGTETPRSLSYGAIYVGHETHGPDNG 590  
 Db 525 SMTPOVNAVYLPKNEIYFPAGILQAPFY-ARNHPRKALNFGGIGVWGMHETLHAEDOG 583  
 QY 591 RKYDNGNDPMMWSTSESEKFEKTKCMINOYSNYWKAGLVKGRITGENIADNG 650  
 Db 584 REYKESGNLRPMWONESLAFRNHTACMEQYNOY--QVNGERLNGRQTIENITDNG 641  
 QY 651 REAFRAYRWINDROGLEPILPGITFTNNOLFSLTAHVRCNSYRPEARQVOIGAH 710  
 Db 642 KAAVNAVYKAWL--RKHG-EEQOLPAVGLTNHOLFVFGAOWCVSVPRESSHEGLVTDPH 698  
 QY 711 SPPOFRVNGAISNSEEFQKAFNCPNPNSTNRGMDSCRLM 749  
 Db 699 SPARFVLTGLSNSRDLRHFEGCPVGSPPMNG-QLCEVW 736

RESULT 7  
 US-10-174-590-420  
 ; Sequence 420, Application US/10174590  
 ; Publication No. US2003008352A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3430R1C42  
 ; CURRENT APPLICATION NUMBER: US/10/174,590  
 ; CURRENT FILING DATE: 2002-06-18  
 ; Prior application removed - See file wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 420  
 ; LENGTH: 736  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-174-590-420

Query Match 30.9%; Score 1223; DB 9; Length 736;  
 Best Local Similarity 35.2%; Pred. No. 3e-91;  
 Matches 267; Conservative 145; Mismatches 307; Indels 40; Gaps 18;  
 QY 2 EAETGSSV--ETGKKANRGTRIAL-VFVVGGLVLTILF--LVSQGL-LSLQAKOEYCL 55  
 Db 7 ELGAGSNVGFQKTRQLGSRTOLEVLVAGASILLALLLGGCVALLQVHRODSHTCL 66  
 QY 56 KPECIEAAAILSKVNSVPCDFFRFACDGRWISNNPIEDMPSYVFWLRHNVDLKL 115  
 Db 67 TEACIRVAGKILSLDNGVSPCEDYFQSCGWIIRNPLDGRSRWNTFNSLMDQNOAIL 126  
 QY 116 KELLEKSISSRRDTEALQKAKILVSSCMNEKAIEKADAKPLHLIRHSPRWPLESNTG 175  
 Db 127 KHLLENT-TFNSSSEAFQKQRFELSLQYERIFELGAQPLRDLI-----EKIG 174  
 QY 176 P---EGWSEKRSLSLQTLATFRQYNSVFIIRLYSPDDKASNEHLIKLDAQATLSLAVR 232  
 Db 175 GWNITGWDQDNF--MEVLKAVAVGTYRATPFYFVYISADSKSSNSNVIGVQDGLFLPSR 232

QY 233 EDYDNSTEANSYRDALYKFWADGAVILLGANSRAEDHDKSVLRLEKIAEMIPH-ENR 291  
 Db 233 DYLL-NRTANKEVLTVALDYMEELGMLGGRPTSTRBOQOVVLELEIOLANITVPQQR 291  
 QY 292 TSEAMYNMNTSELAMIPQDMGLYIKVYIDTLYLHNDISSENVYRVQYFEDLF 351  
 Db 292 DEEKYHMSISEIQLALPSMDWLEFLSLISP-----LELSDEPVVYGYMDYLOQVS 345  
 QY 352 RILGSEKRTIANYLVWVMYRSRIPNLSRPFQWLEFSRYOET-TTLLPOMDKVNF 410  
 Db 346 ELINRTEPSILANNLILNVLQKTTSSIDRRPESQOEKLELTYTKSCVPRMOTCISNT 405  
 QY 411 ESALPYVGMKMFVYFOEDKEMMEELVEGVMAFIDMLEKENEMWADGTRKAKERAR 470  
 Db 406 DDLGFGALGSLFKATFDROSKETIAEGMISEIRAFEEAL-GOLVWMDKTRQAARERAD 464  
 QY 471 AVIAKGYEELTMDTHVEDLKAIFSEADYFGVNLQTRKYLAOSDFEFLRAVPTKEM 530  
 Db 465 AIYDMIGFDFLEPKELDDYDGEISEDSFQNMNLNYSAKVMADQLRPPSRDOW 524  
 QY 531 FTNPDTNAYFASSTNOIREPAGELQKPFWGTETPRSLSYGAIYVGHETHGPDNG 590  
 Db 525 SMTPOVNAVYLPKNEIYFPAGILQAPFY-ARNHPRKALNFGGIGVWGMHETLHAEDOG 583  
 QY 591 RKYDNGNDPMMWSTSESEKFEKTKCMINOYSNYWKAGLVKGRITGENIADNG 650  
 Db 584 REYKESGNLRPMWONESLAFRNHTACMEQYNOY--QVNGERLNGRQTIENITDNG 641  
 QY 651 REAFRAYRWINDROGLEPILPGITFTNNOLFSLTAHVRCNSYRPEARQVOIGAH 710  
 Db 642 KAAVNAVYKAWL--RKHG-EEQOLPAVGLTNHOLFVFGAOWCVSVPRESSHEGLVTDPH 698  
 QY 711 SPPOFRVNGAISNSEEFQKAFNCPNPNSTNRGMDSCRLM 749  
 Db 699 SPARFVLTGLSNSRDLRHFEGCPVGSPPMNG-QLCEVW 736

RESULT 8  
 US-10-176-758-420  
 ; Sequence 420, Application US/10176758  
 ; Publication No. US2003008353A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3430R1C104  
 ; CURRENT APPLICATION NUMBER: US/10/176,758  
 ; CURRENT FILING DATE: 2002-06-21  
 ; Prior application removed - See file wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 420  
 ; LENGTH: 736  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-176-758-420

Query Match 30.9%; Score 1223; DB 9; Length 736;  
 Best Local Similarity 35.2%; Pred. No. 3e-91;  
 Matches 267; Conservative 145; Mismatches 307; Indels 40; Gaps 18;  
 QY 2 EAETGSSV--ETGKKANRGTRIAL-VFVVGGLVLTILF--LVSQGL-LSLQAKOEYCL 55  
 Db 7 ELGAGSNVGFQKTRQLGSRTOLEVLVAGASILLALLLGGCVALLQVHRODSHTCL 66

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Db 7 ELGAGSNVGFQKTRQLGSRTOLEVLGASLLIALLLCLVLAQVYHRDPSHSTCL 66
Oy KPECIEAAALISKVNLVSDPCDNFFPACDGMISNNPDPEDMPSYGVYVWLRHNVDLKL 115
Db 67 TEACIRVAGKILIESLDGVSCEDEYFQSCGMIIRNPLPDGSRKWNFTNSLMDQNALIL 126
Oy 116 KELLEKISRRRDPTEAIOKALILYSSCMNEKAIEKADAKPLHLIRHSPFWPLESNIIG 175
Db 127 KHLLENT-TFNSSSEAEKTOGRFLYSLQVERIEELGAQPLRDLI-----EKIG 174
Oy 176 P---EGVWSEKESLLOTLATFRGOYSNVSFIRLYVSPDDKASNEHLIKLDAQATSLAVR 232
Db 175 GWNITGPMQDNF--MEVLKAAGTYRATPFYVYISADKSSNSNVYQVDSGLFLPSR 232
Oy 233 EDYLDNSTEAKSYRDALYKFPVDTAVLLGANSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
Db 233 DYLL-NRTANEKVITAYLDYMEELGMLGGRPTSTREMOQVLELEIOLANTIVPQDQR 291
Oy 292 TSEAMYNKMNISELSAMIPQFDMIGYIKKVIDTRLYPHLKDISPENYVVRVPOYKDLF 351
Db 292 DEKTIYHKMSISELOALAPSDMWFLEFLSLP-----LELSDSEPVVYGYMDYLOQVS 345
Oy 352 RIIGSERKKTIANLYVMRWYSRIPNLSRRQYRWLEFSVIGOT-TLLPQMDKCVNFI 410
Db 346 ELINRTEPSILNNYLIMNLVOKTSSLDREFSAQEKLETLTYGKKSCVPRMOTCISNT 405
Oy 411 ESALPYVVGKMFVDYFQEDKKEMBELVEGVRAFIIDMLEKENEMDAGTKRKAKEAR 470
Db 406 DDLGALGSLFVKATFGRQSKIEAGMISEIRTAFEEL-GOLVWMDKTRQAAKEKAD 464
Oy 471 AVLAKEGYPEFIMNDTHVEDLKAIFSEADYFENVLOTQRYLAOSDFWMLRKAVPTEW 530
Db 465 AIYDMIGFDFLEKEDLDYDGEISDSFQNMNLNYSKAVMADQLKPPSRDQW 524
Oy 531 FTNPPTVNAFYASATNOIFRPAGELOKPFWGTETPRSLSYGALGVYGHETHEGDNNG 590
Db 525 SMTPOTVNAAYYLPTRKNEIVFPAGILOAPFY-ARNHPKALNFGGIGVVMGHETLTHAFDQ 583
Oy 591 RKYDKNGMLDPWMTSESEKFEKTCMIMNOYSNYMKKAGLVNKGKRLGENTADNGSL 650
Db 584 REYDEKGNLRPWNQNESLAARFNRHTACMEQYNOY--QVNGERLNGRQTLGENTIDNGSL 641
Oy 651 REAFRAYRKWINDRQGLEEPLLPGLTPTNNQLEFLSYAHVRCONSTRPPEAREQVOIGAH 710
Db 642 KAAVNAAYKAML--RKHG-EEQOQLPAVGLTNHQLFFVGFAQVWCVTRPSSHEGLVDPH 698
Oy 711 SPPOFRVNGAISNSEEFQKAFNCPNSTMNGMDSCLRW 749
Db 699 SPARFRVLGTLNSRDLRHFHGCPCVSPMANG-QLCEVW 736

RESULT 9
; Sequence 420, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm

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; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-175-737-420

Query Match      30.9%; Score 1223; DB 9; Length 736;
Best Local Similarity 35.2%; Pred No. 36-91;
Matches 267; Conservative 145; Mismatches 307; Indels 40; Gaps 18;

Oy 2 EAETGSSV-ETGKRNAGTRIAL-VVYGGTLVLTILF--LYSGL-LSLQAKQETCL 55
Db 7 ELGAGSNVGFQKTRQLGSRTOLEVLGASLLIALLLCLVLAQVYHRDPSHSTCL 66
Oy 56 KPECIEAAALISKVNLVSDPCDNFFPACDGMISNNPDPEDMPSYGVYVWLRHNVDLKL 115
Db 67 TEACIRVAGKILIESLDGVSCEDEYFQSCGMIIRNPLPDGSRKWNFTNSLMDQNALIL 126
Oy 116 KELLEKISRRRDPTEAIOKALILYSSCMNEKAIEKADAKPLHLIRHSPFWPLESNIIG 175
Db 127 KHLLENT-TFNSSSEAEKTOGRFLYSLQVERIEELGAQPLRDLI-----EKIG 174
Oy 176 P---EGVWSEKESLLOTLATFRGOYSNVSFIRLYVSPDDKASNEHLIKLDAQATSLAVR 232
Db 175 GWNITGPMQDNF--MEVLKAAGTYRATPFYVYISADKSSNSNVYQVDSGLFLPSR 232
Oy 233 EDYLDNSTEAKSYRDALYKFPVDTAVLLGANSRAEHDMKSVLRLEIKIAEIMIPH-ENR 291
Db 233 DYLL-NRTANEKVITAYLDYMEELGMLGGRPTSTREMOQVLELEIOLANTIVPQDQR 291
Oy 292 TSEAMYNKMNISELSAMIPQFDMIGYIKKVIDTRLYPHLKDISPENYVVRVPOYKDLF 351
Db 292 DEKTIYHKMSISELOALAPSDMWFLEFLSLP-----LELSDSEPVVYGYMDYLOQVS 345
Oy 352 RIIGSERKKTIANLYVMRWYSRIPNLSRRQYRWLEFSVIGOT-TLLPQMDKCVNFI 410
Db 346 ELINRTEPSILNNYLIMNLVOKTSSLDREFSAQEKLETLTYGKKSCVPRMOTCISNT 405
Oy 411 ESALPYVVGKMFVDYFQEDKKEMBELVEGVRAFIIDMLEKENEMDAGTKRKAKEAR 470
Db 406 DDLGALGSLFVKATFGRQSKIEAGMISEIRTAFEEL-GOLVWMDKTRQAAKEKAD 464
Oy 471 AVLAKEGYPEFIMNDTHVEDLKAIFSEADYFENVLOTQRYLAOSDFWMLRKAVPTEW 530
Db 465 AIYDMIGFDFLEKEDLDYDGEISDSFQNMNLNYSKAVMADQLKPPSRDQW 524
Oy 531 FTNPPTVNAFYASATNOIFRPAGELOKPFWGTETPRSLSYGALGVYGHETHEGDNNG 590
Db 525 SMTPOTVNAAYYLPTRKNEIVFPAGILOAPFY-ARNHPKALNFGGIGVVMGHETLTHAFDQ 583
Oy 591 RKYDKNGMLDPWMTSESEKFEKTCMIMNOYSNYMKKAGLVNKGKRLGENTADNGSL 650
Db 584 REYDEKGNLRPWNQNESLAARFNRHTACMEQYNOY--QVNGERLNGRQTLGENTIDNGSL 641
Oy 651 REAFRAYRKWINDRQGLEEPLLPGLTPTNNQLEFLSYAHVRCONSTRPPEAREQVOIGAH 710
Db 642 KAAVNAAYKAML--RKHG-EEQOQLPAVGLTNHQLFFVGFAQVWCVTRPSSHEGLVDPH 698
Oy 711 SPPOFRVNGAISNSEEFQKAFNCPNSTMNGMDSCLRW 749
Db 699 SPARFRVLGTLNSRDLRHFHGCPCVSPMANG-QLCEVW 736

RESULT 10
; Sequence 420, Application US/10173706
; Publication No. US2003002293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey

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QY 531 FTPTTVAEFSASNRNFRPAGELQPFEMGTGXPSSLSGAGVGVYGHFTGFPNNG 530
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 525 SMTPTVTAATLPTKNEVTFVPAAGLLQAFY-ARNHPALNFGGIGVYMGHEHTHAFDDG 5633
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
QY 591 RKYDKNGNLDVPMWSTESSEKFEKTKCMINOYSNYWKRAKJANVKGRKTGENTADNGL 650
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 584 REYDEGNLRPMQWNESTLAARFNHTACMEQYNY--QVNGERLNGQTLGENTIDNGL 6411
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
QY 651 REAFPAAYKKMYNDRROGIEEPLDEGITTNNOLFSTJAHVNCNSYREAPARBOYGAIH 710
      | : | | | : | : | | | : | : | | | : | : | | | : | : | | | : | :
Db 642 KAAATNAYAAWV--KKHG-EEQQLPAVGLYHNLQLETFVFAQWCVSVTRPSSHGLVDPH 6988
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
QY 711 SPQFRVAGVANSSEEPKAFNCPPNSTMNGDSCRLM 749
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 699 SPARFRVLGTJLNSRDLFRHGGCCVYGSPMMDG-OLCEWV 736
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |

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RESULT 12  
ME-10-175

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OS-10-175-752-420
? Sequence 420: Application US/10175752
? Publication No. US20030022295A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Chen, Jian
? APPLICANT: Desnoyers, Luc
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Pan, James
? APPLICANT: Smith, Victoria
? APPLICANT: Watanabe, Collin K.
? APPLICANT: Wood, William I.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P3430RLC60
? CURRENT APPLICATION NUMBER: US/10/175,752
? CURRENT FILING DATE: 2002-06-19
? Prior Application removed - See File Wrapper or Palm
? NUMBER OF SEQ ID NOS: 612
? SEQ ID NO 420
? LENGTH: 736
? TYPE: PRT
? ORGANISM: Homo Saplen
? OS-10-175-752-420

```

Query Match	30.98;	Score 1223;	DB 9;	Length 736;
Best Local Similarity	35.28;	Pred. No. 3e-91;		
Matches 267;	Conservative 145;	Mismatches 307;	Indels 40;	Gaps 18

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QY      2 EAEOTSSV--EUGKANGNGTRIAL-VYFVGVLGTGLTF--LVYQGL-LSIQAKQEXCL 55
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      7 ELGAGSNNGFOGRTROLLGSRHTQLEIYLALCAASLTLAALLGGVIALGVYHHDPSHTCL 66
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      56 KECEIEAAALISKVNLSVDCDNFFRACDGMISNNPIPECMPSXGVYPMLRHNVDLKL 115
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      67 TEACIRVAGKILIESIDRVSCEDFYFSGCGIIRANPIPDGRSKMNTFNSIMQOAIL 126
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      116 KELLEISIRRRDEATQAKIILYSSCMNKAKATEKADAPLHLIHRSFPMFVLESNG 175
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      127 KHLLENT-TFNSSBAEQTKRFLYLSQLOYERIEELGAQPLADLI-----EKIG 174
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      176 P---BCWSEKRFSLQTLATFRCQISNSYFIRLYVSPDDKASNEHLIKLDQATLSLAVR 232
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      175 GNNITGPMDOONF--MEVLKAVAGTYRATPFYFVYISADSKSSNSGNYVQSGSLPSR 232
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      233 EYLDSNGTEAKSYRDALYKFEVNDVAVILLGANSRAEHDKSVLRLEITIAETIMPH--ENR 291
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      233 DYTL-NRTANRKYLVTAIYDVEELGMLGGRPTSTREQOQYLELEIOLANIYVPOQRR 291
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      292 TSEAYNNKMSIELSAMIPQDMVLGYKKYKIDTRLVPHLKDISEPVENYAVPYFNDLF 351
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      292 DEBKTYHKMSISEIQLALFASMDNLEIFSLTSLP-----LEISDSEPVYVYGMNDYLDQVS 345

```

```

OY 352 RIGSEKRTKJANYLVMMVMSRIPJNSRROYLMEESRVOQT-TLLPOMDKCNFI 410
Db 346 ELINTESILNLIYMWUVOKTSSIDLRRESQOEKILETLVTKKSCVPRMOTCISNT 405
OY 411 ESALPYVVKMFVDYQEDERKEMMELVEGVNAFIDMLEKENEMNADGKRRKAKKAR 470
Db 406 DDALFALGSLFVKATFDRQSKETAEGMISITPAFEBAL-GQLVMDKTRQAKKAD 466
OY 471 AVLKVGPEEIMDTHNEDLKAKTSEADYPENVIQTRYLAOSPFMLKRAVPKTEW 530
Db 465 AIYDMGPPDILPEKEDVDYDGEISESESFQNMNLNFSKAVADOLRRPSPDOW 524
OY 531 FTNPFTVAEFSASTNOJIRPAGELOKPEFWEFGTSPSLSGALGVYVHEHTFFPNNG 590
Db 525 SMTQOTVAAVYLLPKINELVEPAGLQAPFY-ARHHPALNFGGIGVYMGHELTNAPDDOG 583
OY 591 RKYDKNGNLDPMWSTESBEKREKTKCMINOYSNYWKKAGLVKGRKTIGENIADNGSL 650
Db 584 REYREKGNILRPMQONESIAAFRHNTHACMEQYNDQ-QVNGERLNGRQTLGENITNDGGL 641
OY 651 READRAYRKVJNDRROGLEEPLFGITFTNNQOLFELSYAHRCNSYRPEARBOVOIGAH 710
Db 642 KAAANAYKAWL--RKHG-EBEQOLPVALVLIHQLFVEFAGVWCVSVPRTPSSHGLVTDPH 698
OY 711 SPQOFVWVAGLSINSEFOKAFNCNPNSTNMGMDSCGLM 749
Db 699 SPAPFRVLGILSNRDLRHRGCGCVGSPMNDG-QLCEWV 736

```

RESULT 13  
NS-10-176

```

? Sequence 420, Application US/10176482
? US-10-176-482-420
? Publication No. US20030022296A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Chen, Jian
? APPLICANT: Desnoyers, Luc
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Pau, James
? APPLICANT: Smith, Victoria
? APPLICANT: Watanabe, Colin K.
? APPLICANT: Wood, William I.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? ACIDS ENCODING THE SAME
? FILE REFERENCE: P3430R1C70
? CURRENT APPLICATION NUMBER: US/10/176,482
? CURRENT FILING DATE: 2002-06-20
? Prior Application removed - See File Wrapper or Palm
? NUMBER OF SEQ ID NOS: 612
? SEQ ID NO 420
? LENGTH: 736
? TYPE: prt
? ORGANISM: Homo Sapien
? US-10-176-482-420

```

Query Match	30.9%;	Score 1223;	DB 9;	length 736;
Best Local Similarity	35.2%;	Pred. No. 3e-91;		
Matches 267;	Conservative 145;	Mismatches 307;	Indels 40;	Gaps 18

[illegible]

```

Db 127 KHLLENT-TFNSSSEAEOKTOREFLYSLQVRIEELGAQPLRLDI-----EKIG 174
Qy 176 P---EGWSEERKPSLLQTLATFRGOYSNVSFIRLYVSPDDKASNEHILKDOATLSIAVR 232
Db 175 GWNITPMDQDNF--MEVKA VAGTYRATPEFTYISADSXSNSNVIQVDSGLFLPSR 232
Qy 233 EDYLDNSTEAKSYRDALYKFNVDYAVLLGANSRAEDHMSVLRLEIKIAEIMIPH-ENR 291
Db 233 DYLL-NRTANEKVLTAYLDYMEELGMLGGRPTSTREQMOQVLELEIQLANTIVYPODQR 291
Qy 292 TTSAMNKNMISLSAMITQFDMLYIKKYIDTRLYPHLKDISPSENVVVRVQYFKDLF 351
Db 292 DEKTIYHKMSISELQALAPSMIDLEFLSLSP-----LELSDSEPVVYVGYMDYLOQVS 345
Qy 352 RILGSEKRTKIANTLYVWRVYSRIPNLSRRFOYRWLEFSRYIOGT-TTLLPQMDKCVNFI 410
Db 346 ELINREPSILNNYLTIMLVOKTSSLDNRRESAQEKLEITLYGTKKSCVPRMOTCISNT 405
Qy 411 ESALPYVVGKMFVDYVFOEDKKEEMELVEGVRAFDIMLEKENEMWDAGTKRKAERAR 470
Db 406 DDALGFALGSLFVKATFDROSKETAEAGMISEIRTAFEAL-GQLVWMDKTRQAKKAD 464
Qy 471 AVLAKEYGPEFIMNDYHVEDLKAIFESADYFGNVLTQRTKLAOSDFWLRKAVPKTEM 530
Db 465 AITDMIGFDFEILPEKELDYDGYEISDSFQNMNLNFSAKYVADQLKRPSPDQW 524
Qy 531 FTNPVTYNAFYSTNQIRFPAGELQKPFPGWGTETPRSLSYGAIGVYGHFTGPDNNG 590
Db 525 SMTPOVNAVYYLPTKNEIYFPAGILQAPFY-ARNHPRKALNFGGIGVYMGHELTTHAFDDG 583
Qy 591 RKYDKNGNIDPWWSTSESEKEKTKCMINQYSNYWKAGLVNKGRTIGENIADNGL 650
Db 584 REYDKNGNLRPMWONESLAFRNHTACMEQYNOY--QVNGERLNGRQTLGENITDNGL 641
Qy 651 REAFRAYRWINDRQGLEPILPGITFTNNQLEFLSYAHVRCNSYRPEARQVOIGAH 710
Db 642 KAAVNAVYKWL--RKHG-EEQQLPAGVLGTLNHLFEVGFAGVWC SVRTPESHGELVTDPH 698
Qy 711 SPPOFRVNGAISNSEFOKAFNCPNSTNMRCMDSCRLM 749
Db 699 SPARFRVLGTLNSRDLRHRFGCPVGPSPMNPQ-QLCEVW 736

RESULT 14
US-10-176-757-420
; Sequence 420, Application US/10176757
; Publication No. US2003002297A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jitan
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C86
; CURRENT APPLICATION NUMBER: US/10/176,757
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-757-420
Query Match 30.9%, Score 1223, DB 9, Length 736.

```

```

Best Local Similarity 35.2%; Pred. No. 3e-91;
Matches 267; Conservative 145; Mismatches 307; Indels 40; Gaps 18;

Qy 2 EAETGSSV-ETGKANNGRIAL-VVFGTLYGLTF--LVYSQGL-LSIAQAOEYCL 55
Db 7 ELGAGSNVGFQKGTROLLGSRTQLELVLAGASLLALLGLGCVAVLQYHRDPSHSTCL 66
Qy 56 KPECEAAALILSKYNLSVDPDCNFFRACGGMISNNPIPEDMFSYGYVPLRNVDLKL 115
Db 67 TEACIRVAGKLTLESIDRVSCEDEYOFSCGGMTRNDPLDGRSRWMTFNSLMDQOAIL 126
Qy 116 KELEKSISRRDTEAIOAKITVSCSNKEAKKADAPLHLIRSPRWPLAESNIG 175
Db 127 KHLLENT-TFNSSSEAEOKTOREFLYSLQVRIEELGAQPLRLDI-----EKIG 174
Qy 176 P---EGWSEERKPSLLQTLATFRGOYSNVSFIRLYVSPDDKASNEHILKDOATLSIAVR 232
Db 175 GWNITPMDQDNF--MEVKA VAGTYRATPEFTYISADSXSNSNVIQVDSGLFLPSR 232
Qy 233 EDYLDNSTEAKSYRDALYKFNVDYAVLLGANSRAEDHMSVLRLEIKIAEIMIPH-ENR 291
Db 233 DYLL-NRTANEKVLTAYLDYMEELGMLGGRPTSTREQMOQVLELEIQLANTIVYPODQR 291
Qy 292 TTSAMNKNMISLSAMITQFDMLYIKKYIDTRLYPHLKDISPSENVVVRVQYFKDLF 351
Db 292 DEKTIYHKMSISELQALAPSMIDLEFLSLSP-----LELSDSEPVVYVGYMDYLOQVS 345
Qy 352 RILGSEKRTKIANTLYVWRVYSRIPNLSRRFOYRWLEFSRYIOGT-TTLLPQMDKCVNFI 410
Db 346 ELINREPSILNNYLTIMLVOKTSSLDNRRESAQEKLEITLYGTKKSCVPRMOTCISNT 405
Qy 411 ESALPYVVGKMFVDYVFOEDKKEEMELVEGVRAFDIMLEKENEMWDAGTKRKAERAR 470
Db 406 DDALGFALGSLFVKATFDROSKETAEAGMISEIRTAFEAL-GQLVWMDKTRQAKKAD 464
Qy 471 AVLAKEYGPEFIMNDYHVEDLKAIFESADYFGNVLTQRTKLAOSDFWLRKAVPKTEM 530
Db 465 AITDMIGFDFEILPEKELDYDGYEISDSFQNMNLNFSAKYVADQLKRPSPDQW 524
Qy 531 FTNPVTYNAFYSTNQIRFPAGELQKPFPGWGTETPRSLSYGAIGVYGHFTGPDNNG 590
Db 525 SMTPOVNAVYYLPTKNEIYFPAGILQAPFY-ARNHPRKALNFGGIGVYMGHELTTHAFDDG 583
Qy 591 RKYDKNGNIDPWWSTSESEKEKTKCMINQYSNYWKAGLVNKGRTIGENIADNGL 650
Db 584 REYDKNGNLRPMWONESLAFRNHTACMEQYNOY--QVNGERLNGRQTLGENITDNGL 641
Qy 651 REAFRAYRWINDRQGLEPILPGITFTNNQLEFLSYAHVRCNSYRPEARQVOIGAH 710
Db 642 KAAVNAVYKWL--RKHG-EEQQLPAGVLGTLNHLFEVGFAGVWC SVRTPESHGELVTDPH 698
Qy 711 SPPOFRVNGAISNSEFOKAFNCPNSTNMRCMDSCRLM 749
Db 699 SPARFRVLGTLNSRDLRHRFGCPVGPSPMNPQ-QLCEVW 736

RESULT 15
US-10-176-913-420
; Sequence 420, Application US/10176913
; Publication No. US2003002298A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jitan
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```



GenCore version 5.1.4-p5.4578  
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# OM protein - protein search, using sw model

Run on: May 21, 2003, 18:45:44 ; Search time 48 Seconds  
(Without alignments)  
1500.098 Million cell updates/sec

Title: US-09-913-955a-1

Perfect score: 3958  
Sequence: 1 MEAFGTSSVETGKRNKGR.....AFNCPPNSTWNRGMDSCRLM 749

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1351	34.1	774	2	JC7265
2	1283.5	32.4	750	1	HYHUN
3	1263.5	31.9	750	1	HYRIN
4	1260	31.8	751	1	HYRBN
5	1257	31.8	758	2	JC2521
6	1257	31.5	770	2	JC4136
7	1248.5	31.5	758	2	A54667
8	1243.5	31.4	754	2	A53679
9	1241.5	31.4	754	2	A47268
10	1184	29.9	825	2	I46078
11	1119.5	28.3	750	2	D88082
12	1014.5	25.6	766	2	T20003
13	997	25.2	590	2	C88099
14	949	24.0	769	2	T24949
15	814.5	20.6	706	2	F87683
16	778	19.7	734	2	T16182
17	672	17.0	663	2	C70838
18	668	16.9	700	2	B82788
19	646.5	16.3	667	2	C87236
20	606	15.3	1589	2	T22668
21	599.5	15.1	732	1	HYHUK
22	567	14.3	798	2	T28906
23	547.5	13.8	801	2	T31991
24	512.5	12.9	726	2	B88099
25	511.5	12.9	823	2	T28132
26	502	12.7	627	2	F53290
27	495	12.5	627	2	C86850
28	494	12.5	627	2	A47098
29	442	11.2	774	2	T31512

30	420	10.6	649	2	E88098	protein F18A12.6 [
31	417	10.5	630	2	B98058	endopeptidase O (E
32	417	10.5	630	2	F95191	hypothetical prote
33	410.5	10.4	534	2	T33020	hypothetical prote
34	379	9.6	684	2	T32024	hypothetical prote
35	365	9.2	564	2	T11548	probable zinc meta
36	350	8.8	651	2	T31513	hypothetical prote
37	335.5	8.5	658	2	T16040	hypothetical prote
38	325.5	8.2	732	2	T32023	hypothetical prote
39	297.5	7.5	817	2	T25758	hypothetical prote
40	297	7.5	570	2	G88098	protein F18A12.3 [
41	291	7.4	734	2	F88098	protein F18A12.4 [
42	195.5	4.9	433	2	T28805	hypothetical prote
43	185.5	4.7	500	2	D88099	protein F18A12.5 [
44	157.5	4.0	198	2	D88098	protein F06D4.5 [1
45	157.5	4.0	198	2	T32025	hypothetical prote

## ALIGNMENTS

### RESULT 1

JC7265  
neprilysin (EC 3.4.24.11) II - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 02-Sep-2000  
C:Accession: JC7265  
R:Tanja, O.; Facchinetti, P.; Rose, C.; Bonhomme, M.C.; Gros, C.; Schwartz, J.C.  
Biochem. Biophys. Res. Commun. 271, 565-570, 2000  
A:Title: Neprilysin II: A putative novel metalloprotease and its isoforms in CNS and  
A:Reference number: JC7265  
A:Contents: Brain and testis  
A:Accession: JC7265  
A:Molecule type: mRNA  
A:Residues: 1-774 <TAN>  
A:Genetics:  
A:Gene: nepril  
C:Superfamily: neprilysin  
C:Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropeptide; testis;

Query Match	34.1%	Score 1351;	DB 2;	Length 774;
Best Local Similarity	38.2%	Pred. No. 1.4e-83;		
Matches 289;	Conservative 156;	Mismatches 266;	Indels 46;	Gaps 18;
QY	18	GTRALVVF--VGGTL-VIGTILF-----LVSGLLSLQAKQECIKPECTEAAATL	67	
DB	39	GAIVTIGVFYSIGKQLPLNSLHVSRRHRTVYKRVLRDSSOKSDICTTPSCYIARATL	98	
QY	68	SKVNLVDPDNEFFRACDGMISNPIPEDMPSYGYVPMLRHNVDLKLELEKISRRR	127	
DB	99	QNDQSKKPCDNYOYACGGMWRHNVIPENSRYSVFDLRDELVLKGVLEDSVQHR	158	
QY	128	DTEALQAKTILYSSCKNEKAEKADAPLHILRHSPFRPVLESNIGEGVWSER--K	184	
DB	159	--PAVEAKTILYSSCKNQSVTEKRDEPLNLV--DWIGGPPVAMDK-----WNETMGK	209	
QY	185	FSLLQTLATFRGQYNSVFIKLVVSPDDKASNHILKLDATSLAVREDYLDNSPEAKS	244	
DB	210	WELEKQLAVNSQPNRRVLIDLEFIWDDQNSKHVLIYIDPITGMSREYTF--KDSNR	267	
QY	245	YRDALYKFNVDYAVL-----LGANSRAEDHKSVLRLEIKIAELIMPHENTTS--EAY	297	
DB	268	VREAVLGFMTSVAPMLRDLNPGEDVLQGEAQLVLETHLANFTVQEKRHVDYALY	327	
QY	298	NKANISLSAM--IPQFDWLGITKRYIDRLVYHLKDISESENVVVRVQYFQDLRIIG	355	
DB	328	HRGLELELQERFGIKGFNMFLFIONVLSVQV---ELAPNEVYVYGGIYENLEIID	383	
QY	356	SERKTTANTLVPMYMYRIPNISRRQYKWLFEFVIOGTITLLQPMQKCVAFISALP	415	
DB	384	VFPQQTQNTLVNVLVDKIGLSQRFKAKRVYKALGTTIEEVRMECVSYVSNME	443	
QY	416	YVVGKMFVDVYFQEDKKEAMEELVEGVRAFIIDLEKENEMWDAGTKRRAKEKARAVLAK	475	



```

Db 444 SAVGLYIKRAFSKDSKSIYSELTEKIRSFVDNLDELIN-WMDESKKKAQEKALNIREQ 502
Qy 476 VGYPEFIM--MDTHNEDLKAIFSEADYFEGNVLTQTRKYLAAQSPDFMRAKVPETWFTN 533
Db 503 IGYPIYILEDNNRHLDEDEYSSLTFSSEDLTFYENGLONNKNNQSLKRLKREKVDNLTIG 562
Qy 534 PTTVAAFYASTNQIRFAGELQKPFEPWGTETPRSLSGAIGVIGHEFTGFDDNGRKY 593
Db 563 AAVVNAFYSPPRNLIVFAGLQPPFF-SKQOPALNNGGIGMVICGHEITHGFDDNGRNF 621
Qy 554 DKNGNLDPMWSTSEBEKKEKTKCMINOYSNVYKKA-GLNVKGRKRLGENIADNGGLRE 652
Db 622 DKNGNLDPMWSTSEBEKKEKTKCMINOYSNVYKKA-GLNVKGRKRLGENIADNGGLRE 681
Qy 653 AFRAVKKWINDROGLEPILPGITFTNNQIFLSTAHVRCNSYRPEARQVIGAHSP 712
Db 682 AKKALQWL---ABGRDQRLPLGLNLTYAQLFNTIYQWCGSYRPEAFIQSITVDVHP 738
Qy 713 POFRVNGAISNSEFOKAFNCPNPNSTNMGDSCLW 749
Db 739 LKRYLIGSLQNLPGFSEAFHCPRGSPMH-PMNRCRIW 774

```

## RESULT 2

```

neprilysin (EC 3.4.24.11) [validated] - human
N:Alternate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase 24.11;
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text, change 08-Dec-2000
C:Accession: A41387; A36173; S05275; JLU084; S00350; S02228
R:Id:Adamo, L.; Shipp, M.A.; Masteller, E.L.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 7103-7107, 1989
A:Title: Organization of the gene encoding common acute lymphoblastic leukemia antigen
A:Reference number: A41387; MUID:8936688; PMID:2528720
A:Accession: A41387
A:Molecule type: DNA
A:Residues: 1-750 <DNA>
A:Cross-references: GB:M26605
A:Note: The authors translated the codon AAC for residues 14 and 72 as Asp
R:Shipp, M.A.; Richardson, N.E.; Sayre, P.H.; Brown, N.R.; Masteller, E.L.; Clayton, L.R
Proc. Natl. Acad. Sci. U.S.A. 85, 4819-4823, 1988
A:Title: Molecular cloning of the common acute lymphoblastic leukemia antigen (CALLA)
A:Reference number: A36173; MUID:88263036; PMID:2368607
A:Accession: A36173
A:Molecule type: mRNA
A:Residues: 1-750 <SH1>
A:Cross-references: GB:J03779
A:Note: part of this sequence was confirmed by protein sequencing
R:Jonigeel, C.V.
Submitted to the EMBL Data Library, August 1988
A:Reference number: S05275
A:Accession: S05275
A:Molecule type: mRNA
A:Residues: 1-750 <ION>
A:Cross-references: EMBL:Y00811; NID:929625; PIDN:CA68752.1; PID:929626
R:Lebarte, M.; Vera, S.; Tran, R.; Addis, J.B.; Onizuka, R.J.; Quackenbush, E.J.; Jong
J. Exp. Med. 168, 1247-1253, 1988
A:Title: Common acute lymphocytic leukemia antigen is identical to neutral endopeptidase
A:Reference number: JLU084; MUID:89010526; PMID:2571756
A:Accession: JLU084
A:Molecule type: mRNA
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 2-191; 211-737 <LET>
A:Cross-references: EMBL:Y00811
A:Note: part of this sequence, including the amino end of the mature protein, was confir
R:McFoy, B.; Khan, W.J.; Seeburg, P.H.; Mason, A.D.; Scholtfield, P.R.
FEBS Lett. 229, 206-210, 1988
A:Title: Molecular cloning and amino acid sequence of human enkephalinase (neutral endop
A:Reference number: S00350; MUID:88152222; PMID:3162217
A:Accession: S00350
A:Molecule type: mRNA
A:Residues: 3-750 <MAL>

```

```

A:Cross-references: EMBL:X07166
A:Note: 467-Thr was also found
C:Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the amide
C:Comment: This antigen is an important cell surface marker glycoprotein in the diag
C:Genetics:
A:Gene: GDB:MME
A:Cross-references: GDB:120190; OMIM:120520
A:Map position: 3q25.1-3q25.2
A:Intron: 54/1; 66/1; 120/1; 147/1; 179/1; 218/3; 240/3; 285/3; 319/3; 365/2; 396/3;
C:Superfamily: neprilysin
C:Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface anti
F:2-750/Product: neprilysin [status experimental <MAT>]
F:16-23/Region: stop-transfer sequence
F:29-51/Domain: transmembrane #status predicted <TM>
F:52-750/Domain: extracellular #status predicted <EXT>
F:145; 285; 311; 325; 335; 628/Binding site: carbohydrate (asn) (covalent) #status predict
F:584; 588/Binding site: zinc (His) #status predicted
F:585/Active site: Glu #status predicted

```

```

Query Match 32.4% Score 1283.5; DB 1; Length 750;
Best local similarity 35.9% Pred. No. 5.2e-79;
Matches 272; Conservative 155; Mismatches 285; Indels 45; Gaps 19;

```

```

Qy 13 KKANRGRALAVYVGTVLGTITFLVSGLLSLQAKOE--CYCKPECTEAAAAILSKV 70
Db 19 KKKQRTPEISLSY--LVL--LTITIVTIALATVYDDGICKSSDCKSAARLIQNM 73
Qy 71 NLSVDCDNFRRACGMSINNPIDPMPSYGYVPLRNVNLDLKELEKISRRPTE 130
Db 74 DATTECTGFEKACGGMKRNVPETSSRYGNFDLRLDELVYLVKDLQ--PTEIDIV 131
Qy 131 AIOKATLIVSSCNEKAIEKADAKPLHLIRSPFVPLESINIPPEGWSER--KPSL 187
Db 132 AVGKAKALRSCINESAIDSRGEPPLKTL-PDYGMPATEN-----WEKYGASMTA 184
Qy 188 LQTLATFPGQYSNVITRLVYSPDOKASNEHLIKDQATLSLAVREDYLDNSTEAKSYRD 247
Db 185 EKAIQDINSKYGRKVLINFLVGGDDKNSVNHVHIDQPLGPR-DYEECTGYEACT 243
Qy 248 ALKFWVDRAVL-----LGANSRAHEMKSVLRREITAIIMPHENRSE-AMYKM 300
Db 244 AYVDFMISARLIRQERPLIDENQALDKMKVMELEKTAIYAKPERNDPMLYKIM 303
Qy 301 NISLSAMT-----POFDMLGIRKVIDTIRLPHLKDIPSENVVVRVQYKDFLRL 354
Db 304 TLAQIONNLSLEINGKPFQMLNFTNINSTVNI---STINEDVYVAPELTAKPIL 359
Qy 355 GSERKRTIANYLVKRVYRIPMLSRFQYRMLESRYVIGTTLLPQMDKVFIESAL 414
Db 360 TKYSARDLQNLMSWRIMDLVSLSTRYKESRNARFKALYGTTSFATWRCANVYNGM 419
Qy 415 PYYVGMFVDYVQEDKRMMEELVGVVATLIDLEKNEKMDAGSTRKAEKARAVLA 474
Db 420 ENNAVGRVLEAFAAGSKHVEDLQIREVFIQTLD-DLTWMDAETKRAEKALAKE 478
Qy 475 KVGYP-EFTMNDTHVEDKAIKFESEADYFGLVLTQTRKYLAAQSPDFMRAKVPETWFTN 533
Db 479 RIGYPPDIYSNNKLNNELELYNKEDDEFENIQLNKAIFSQSKQKLKREKVDNLTIG 538
Qy 534 PTTVAAFYASTNQIRFAGELQKPFEPWGTETPRSLSGAIGVIGHEFTGFDDNGRKY 593
Db 539 AAVVNAFYSPPRNLIVFAGLQPPFF-SAQOSNLNNGGIGMVICGHEITHGFDDNGRNF 597
Qy 594 DKNGNLDPMWSTSEBEKKEKTKCMINOYSNVYKKA-GLNVKGRKRLGENIADNGGLRE 652
Db 598 NNDGDLVDMWTOQASNFREQSQCWYQYGNFSWDLAQGHQHLINTLGENIADNGGLGQ 657
Qy 653 AFRAVKKWINDROGLEPILPGITFTNNQIFLSTAHVRCNSYRPEARQVIGAHSP 712
Db 658 AYRAYQNTI--KKG-EELTLPGDLNKHQPLFLNFAQWCGTYRPEAYVANSIKITVDVHP 714
Qy 713 POFRVNGAISNSEFOKAFNCPNPNSTNMGDSCLW 749

```

Db 715 GNRRIIGTIONSAPFSAFSEAFHCKRKNSTYNN-PEKCRW 750

# RESULT 3

HYRBN

neprilysin (EC 3.4.24.11) - rat

N/Alternate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase 24.11;

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text, change 18-Jun-1999

C/Accession: A29295; A33521

R/Maffroy, B.; Schofield, P.R.; Kiang, W.J.; Seeburg, P.H.; Mason, A.J.; Henzel, W.J.

Biochem. Biophys. Res. Commun. 144, 59-66, 1987

A/Title: Molecular cloning and amino acid sequence of rat enkephalinase.

A/Reference number: A29295; MUID:87213218; PMID:3555469

A/Accession: A29295

A/Molecule type: mRNA

A/Residues: 1-750 <MAL>

A/Note: part of this sequence, including the amino end of the mature protein, was confir

R/Bateman Jr., R.C.; Jackson, D.; Slaughtner, C.A.; Umiltan, S.; Chai, Y.G.; Moomaw, C.;

J. Biol. Chem. 264, 6151-6157, 1989

A/Title: Identification of the active-site arginine in rat neutral endopeptidase 24.11

A/Reference number: A33521; MUID:89197908; PMID:2703483

A/Accession: A33521

A/Molecule type: protein

A/Residues: 95-102, 'X', 104-129 <BAT>

C/Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the amino

ney.

C/Superfamily: neprilysin

C/Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface antigen;

F:9-750/Product: neprilysin #status experimental <MAL>

F:16-23/Region: stop-transfer sequence

F:29-51/Domain: transmembrane #status predicted <TMN>

F:52-750/Domain: extracellular #status predicted <EXT>

F:145,285,325,628/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:311/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:584,588/Binding site: zinc (His) #status predicted

F:585/Active site: Glu #status predicted

Query Match 31.9%; Score 1263.5; DB 1; Length 750;

Best Local Similarity 35.7%; Pred. No. 1.2e-77;

Matches 270; Conservative 151; Mismatches 291; Indels 45; Gaps 19;

Db 13 KKRQMTPEISLSV---LVL--LTTTAVTMAIATYDGIKSSPCISARLIQNM 73

71 NLSVPCDNFRFACDGMISNNPREDMPISGVYPMLRHNVLDLKELESISRRTDE 130

74 DASAPCDDFFKYACGMKLRNVIPETSSRYSNFDLDELVLKVDLQOE--PKTEIV 131

131 AIOKKILYSCMNEKAIEKADAKLHLIRSPFRMYLNSNICEGVSE---RKFSL 187

132 AVOKAKTILYRSCINSASIDSRGGPLTLTL--PDIGWVASQN-----WQTYGTSTWA 184

Db 420 ENAVGLUYEAFAAGSKSHVEDLLIQIREVLTQTLD--LTMWDAETFKKAEKALAIKE 478

475 KGYR-P-EFTMNDTHVEDLKAIKFSADYFGVNLQTRKTLAOSDFEMLRKAPKTEMTN 533

479 RIGYDDIISNENKLNNELELYKEEYFENIOMLKFSQSKLREKDKDEWISG 538

534 PTYNVAFSASTQIREPAGELQPFPGWGTETPRSLSYAIGVIGHEPTGFDNNGRY 593

539 AAVYNFYSGRNQIYFPGIQLDPPF--SARQSNLSNIGIGVICHETTHGFDNGRNF 597

594 DKNGLDPMWSTSEKFEKTKCMINQSYNYWKKA--GLNFKGRTGENTADNGIRE 652

598 NKDGDLVDMWTQOSANNFKDOQSCWYQGNFTWDLAGGSHNGITGENTADNGIQQ 657

653 AFPAIKRWINDRQGLDEPLRPGITTTNNQPLFLSAHRCSYRPEARQVOIGASHP 712

658 AYRAYONYV--KKNG--EKLPLGLDNLHKKQLPFLNLAQVCGTYREYAVNSIKTDVHS 714

713 POFVNGAISNSEFOKAFNCPNSTNRGMDSCLRM 749

715 GNRRIIGTIONSAPFSAFSAFSEAFHCKRKNSTYNN-PEKCRW 750

neprilysin (EC 3.4.24.11) - rabbit

N/Alternate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase 24.

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text, change 18-Jun-1999

C/Accession: A29451; A16872

R/Devallant, A.; Lazure, C.; Nault, C.; Le Moual, H.; Seldah, N.G.; Chretien, M.; Kahn,

EMBO J. 6, 1317-1322, 1987

A/Title: Amino acid sequence of rabbit kidney neutral endopeptidase 24.11 (enkephalin

A/Reference number: A29451; MUID:87275825; PMID:2440677

A/Accession: A29451

A/Molecule type: mRNA

A/Residues: 1-751 <DEV>

A/Cross-references: EMBL:X05338

A/Note: part of this sequence, including the amino end of the mature protein, was con

R/Kahn, P.H.; Powell, J.F.; Beaumont, A.; Rogues, B.P.; Mallet, J.J.

Biochem. Biophys. Res. Commun. 145, 488-493, 1987

A/Title: An antibody purified with a lambda gIII fusion protein precipitates enkephal

A/Reference number: 146872; MUID:87241544; PMID:3297057

A/Accession: 146872

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 207-275 <KAR>

A/Cross-references: GB:M16593; NID:g165556; PIDN:AAA53694.1; PID:g165557

C/Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the am

ney.

C/Superfamily: neprilysin

C/Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface anti

F:2-751/Product: neprilysin #status experimental <MAL>

F:16-23/Region: stop-transfer sequence

F:29-751/Domain: transmembrane #status predicted <TMN>

F:52-750/Domain: extracellular #status predicted <EXT>

F:145,286,312,326/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:585,589/Binding site: zinc (His) #status predicted

F:586/Active site: Glu #status predicted

F:629/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 31.8%; Score 1260; DB 1; Length 751;

Best Local Similarity 36.0%; Pred. No. 2e-77;

Matches 273; Conservative 149; Mismatches 290; Indels 46; Gaps 20;

Db 13 KKRQMTPEISLSV---LVL--LTTTAVTMAIATYDGIKSSPCISARLIQNM 73

19 KKRQMTPEISLSV---LVL--LTTTAVTMAIATYDGIKSSPCISARLIQNM 73

71 NLSVPCDNFRFACDGMISNNPREDMPISGVYPMLRHNVLDLKELESISRRTDE 130

74 DATAEPCDDFFKYACGMKLRNVIPETSSRYSNFDLDELVLKVDLQOE--PKTEIV 131

RESULT 5  
JC2521  
endothelin converting enzyme (EC 3.4.24.-) I, umbilical vein endothelial cell form - human  
C:Species: Homo sapiens (man)  
C:Date: 17-May-1995 #sequence\_revision 14-Jul-1995 #text\_change 20-Jun-2000  
C:Accession: JC2521  
R:Shimada, K.; Matsushita, Y.; Wakabayashi, K.; Takahashi, M.; Matsubara, A.; Iijima, Y.  
Biochem. Biophys. Res. Commun. 207, 807-812, 1995  
A:Title: Cloning and functional expression of human endothelin-converting enzyme cDNA.  
A:Reference number: JC2521; MUID:95169128; PMID:7864876  
A:Accession: JC2521  
A:Molecule type: mRNA  
A:Residues: 1-758 <SHIT>  
A:Cross-references: GB:043698; NID:g1197803; PIDN:BA07800.1; PID:g1197804  
A:Experimental source: umbilical vein endothelial cells  
C:Genetics:  
A:Gene: GDB:ECEL1; ECE  
A:Cross-references: GDB:698357; OMIM:600423  
A:Map position: 1p36.1-1p36.1  
C:Superfamily: neprilysin  
C:Keywords: alternative splicing; glycoprotein; hydrolase; metalloproteinase; transmembrane  
F:51-77/Domain: transmembrane #status predicted <TM>  
F:154\_175\_198\_258\_304\_350\_371\_527\_620\_639/Binding site: carbohydrate (Asn) (covalent) #status  
F:595\_599/Binding site: zinc, catalytic (His) #status predicted  
F:356/Active site: Glu #status predicted

Best local similarity 37.6%; Pred. No. 3.3e-77;  
Matches 281; Conservative 126; Mismatches 276; Indels 64; Gaps 21;

```
QY 21 IALVYVGGTLVLTGLLEFLVSGCLSLQAKOEYCLKPECIEAAAILSVNLSVDPDNF 80
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 VLVLVV-----LAAGLVACLAALGLOYOTRSPVCSICSEACVSYSILSSMDPLVPCGHF 113
QY 81 FRPACGWSINNPIDPDMSESYGVYPMLRHHVVDLTKLLEKLSISRRDDEALQAKILS 140
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 FSVACGWMKANVPDGHGRWGFNFSLMHEHQAIIHLLFNSTA--SVSEAERKAQVYR 171
QY 141 SCMEKAIEKADAKPLLHLRHSPPFRVPVLESNIGEGVSEKTSLLQTLATFRGOYSN 200
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 ACMEHRIEELRAKPLMELIERLG-GWNI-----TGPWAKDNFQ--DTLOVYAHNYR 221
QY 201 SVYIRLYVSPDDKASNEHLKIDQATLSLAVEDYLDNSTEAKSTYDALKRMVDTAVLL 260
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 222 SPFFSYVASDKSNSSNVIYQDSGLSPSDYTL-NKTEKVLTYGLANTVOLGKLL 280
QY 261 GANSSRA-EHDKSVLRLEIKIAELMIPHEMNTSEAM-YKNKNSIELSAMIPQFMLGYT 318
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 281 GGGDEFAIRPQQOILDFETALANITIPQEKRRDELIYHKVTAELQTLAVAINMLPE- 339
QY 319 KAVYDRLPLHKDISPSENVVVRVQYFKDLFRILIGSRKKTIANLYLVWRVYSRIPVL 378
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 340 ---LNTIFP--VEINSEPIVYDYDEYLEQSTLINTDRLCLNNYIMNLVYRTSSEL 394
QY 379 SRRFOYRMLEFSRVIOGT--TTLPLQWDKCVNTEESALPYVGMKMFVDYFQEDKEMME 437
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 395 DQFQDADKEFMEVNYGTRKTCCLPRKKFVDSPTENNLLGALDPMYKAFAPDSSIAIE 454
QY 438 LVEGVMAIIDLKENEWMDAGTRKAKERAVLAKYGEFTY-----NDTHV 488
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 455 ILLEIKKAEESL-STLKMDEDETRSAKEKADAIYMGYDNFTMDPELKDVENDYTA 513
QY 489 NEDLKAIFKSEADYEGCNVLOTKRKYLAQSDPEF-----LRKVPKTEWNTNPTYNAPFS 542
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 514 VVDL-----YENAMRF-----EYFSKRVATADQLRKAPNDQSMTPMNAIYIS 558
QY 543 ASTNQIRFPAGELQKRFPEWGTEYPRLSLSYGAIGVIVGHEFTGFDNNGRKYDKGNLDPW 602
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 559 PKRNEIVFPAGILQAPFYRRS-PKALNCGGIGGVVGHETLHAFDQDGREYDKDGNLNPW 617
QY 603 MTESESEKKEKTKMINDYNSYYMKKAGLANKGKRTIGENTADNGLEAPRAYRAKRN 662
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 618 WKNSSVEAKRQTECHVEQYSNY--SVNGEPNAGRHTTGENTADNGGKAAARAYQANNV- 674
QY 663 DRQGLEEPLDGLGITFNNQLFFLSYAHRCNSYSPREAREQVIGASPPQFNRGASIS 722
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 675 -KKNGAERS-LFTLGILTNNQLEFFLGAQYWCVCVRPESHGELIIDPHSPSFRYIGLS 732
QY 723 NSEFQAKFNCPPNSTANRGMDSCRLM 749
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 733 NSEKSEHFRCPGPPSPMN-PPHKCEVW 758
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
JC4136
endothelin converting enzyme (EC 3.4.24.-) 1, renal adenocarcinoma form - human
C:Species: Homo sapiens (man)
C:Date: 31-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C:Accession: JC4136; S51009; S47269
R:Yoritsumu, K.; Moroi, K.; Inagaki, N.; Saito, T.; Masuda, Y.; Masaki, T.; Saito, S.;
Biochem. Biophys. Res. Commun. 208, 721-727, 1995
A:Title: Cloning and sequencing of a human endothelin converting enzyme in renal aden
A:Reference number: JC4136; MUID:95209687; PMID:7695628
A:Accession: JC4136
A:Molecule type: mRNA
A:Residues: 1-770 <YOR>
A:Cross-references: GB:D949471; NID:6695404; PION:BAA08442.1; PID:6695405
A:Experimental source: renal adenocarcinoma cell
A:Note: It is uncertain whether Met-1 or Met-18 is the initiator
R:Schmidt, M.; Kroeber, B.; Jacob, E.; Seuburger, H.; Subkowski, T.; Otter, R.; Meyer
```

FEBS Lett. 356, 238-243, 1994  
 A:Title: Molecular characterization of human and bovine endothelin converting enzyme (EC  
 A:Reference number: S51009; MUID:95104423; PMID:7805846  
 A:Accession: S51009  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 18-770 <SC2>  
 A:Cross-references: EMBL:Z55307; NID:G535181; PIDN:CAA84548.1; PID:G535182  
 C:Comment: This enzyme is a phosphoramidon-sensitive, membrane-bound metalloprotease.  
 C:Genetics:  
 A:Gene: GDB:ECEL1; ECE  
 A:Cross-references: GDB:698357; OMIM:600423  
 A:Map position: 1p36.1-1p36.1  
 C:Superfamily: neprilysin  
 C:Keywords: alternative splicing; glycoprotein; hydrolase; metalloproteinase; phosphop  
 F:69-89/Domain: transmembrane #status predicted <TM>  
 F:25/Binding site: phosphate (Thr) (covalent) #status predicted  
 F:166,187,210,270,316,362,383,539,632,651/Binding site: carboxylate (Asn) (covalent) #  
 F:607,611/Binding site: zinc, catalytic (His) #status predicted  
 F:608/Active site: Glu #status predicted

Query Match 31.8%; Score 1257; DB 2; Length 770;  
 Best Local Similarity 37.6%; Pred. No. 3,4e-77;  
 Matches 281; Conservative 126; Mismatches 276; Indels 64; Gaps 21;

QY 21 IALVFGVGLVLTIFLVSQGLSLQAKQVCLKPCIEAAALISKVLSVPCDNF 80  
 DB 70 VLVVLVLAAGVLAALAGVLTQYOTRSPVCLSEACSVTSSLSMDPTVPCDF 125  
 QY 81 FFAACDGIWNNPIEDMPSYGVFWLHNDLKLKELLEKSISRRTDAIQAKILYS 140  
 DB 126 FSYACGMIKANPYDDGHSRGTFSNLMEHQALIKHLENSTA--SVSEAKRAQYYR 183  
 QY 141 SCMKAEKADARPLHLIHLSPFRWVLESNIGPEVWSEKRFSLQTLATRGQYSN 200  
 DB 184 ACMNTRIEELRAKPLMLIELRLG-GWNI-----TGPMAKDNFQ--DTLQVVTAAHRT 233  
 QY 201 SFVILYSPDDKASNEHLKLDQATLSLAVREDYLDNSTAKSYRDALYFMVDTAVLL 260  
 DB 234 SPFEVYVSADSKNSNSNVIOVDSGLGPSRDYLL-NKTENEKVLTOGLYMMVQGLKLL 292  
 QY 261 GANSSRA-EHDMKSVLRLEIKIAETIMPHENTSEAM-YNNKNISELSAMIPQDMGLYI 318  
 DB 293 GGGDEEARIPMOQILDEFETALANTITIPQEKRRDELLYHKYTAELQTLAPAIWMLPF- 351  
 QY 319 KKVIDRIYPLHKDISPENNVVVRPOYFKDLFRILGSEKRTIANTLYMMRVYSRIPLN 378  
 DB 352 ---LNTIYFP--VEINSEPIVYDKETLEQISTLINTDRCLLNMYIMLVKRTSSEL 406  
 QY 379 SRRFQRMLEFSRVIOGT-TLLLPQMDKCNFIESALPYVVGKMFVDYVFOEDKEMEE 437  
 DB 407 DQRPDADAEKFMVWYGTCKTCLPRMKFCVSDTENNLGAFALGPMVKAFTFADSKSTATE 466  
 QY 438 LVEGVRAFIDMLEKENEMDAGTKRKAERAVLAKYGFPEFTM-----NDTHV 488  
 DB 467 ILLEIKKAFEEESL-STLKMDEETRKSAKERADALYNNIGYDNFTMDKEIDKYENDNTA 525  
 QY 489 NEDLKAIFSEADYGVNLTQTKRYLAQSDFFM-----LRKAVPTMEFTNPTVNAFYS 542  
 DB 526 VPDL-----YFENMRP-----FNFESWRVTADOLKRAKPNDDQSMTPPMVNAFYS 570  
 QY 543 ASTNOIRPAGELQKPFPMGTETPRSLSYGAIGVIVGHEFTGFDNNRKNKDKNGNDLPW 602  
 DB 571 PKKNITVPAGITQAPFYTRBS-PKALNFGIGVYVGHETLHAPDQGRREYDKDGNLAPW 629  
 QY 603 WSTESEKFEKTKCMINQYSNYWKAGLVAKKRTGEMINADNGILREAFRAYRKAIN 662  
 DB 630 WKNSSVEAFKROTCMVBOYSNY--SVNGEPVNGRHTIGENIADNGISKAAYRAYQNNV- 686  
 QY 663 DRQGLEELPLGTFTNNOLFSLYAVHRCNSYRPEARAOVQGAASPOFRNGAIS 722  
 DB 687 -KKNGAHS-LPTGLTNNQLFTLGAQVWCSTRTPESSHGLITDPHSRFRVIGSL 744

QY 723 NSEFOKAFNCPNSTMNGMDCRLM 749  
 DB 745 NSEFSEHRCPPGSPMN-PPKCEVM 770

## RESULT 7

endothelin converting enzyme (EC 3.4.24.-) 1 - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Nov-1999  
 C:Accession: A54667; JC2448  
 R:Xu, D.; Emoto, N.; Giald, A.; Slaughter, C.; Kaw, S.; demit, D.; Yanagisawa, M.  
 Cell 78, 473-485, 1994  
 A:Title: ECE-1, a membrane-bound metalloprotease that catalyzes the proteolytic activ  
 A:Reference number: A54667; MUID:94340737; PMID:8062389  
 A:Accession: A54667  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-758 <XUA>  
 A:Cross-references: GB:U27342; NID:9897601; PIDN:AAA82928.1; PID:9897602  
 R:Ikura, T.; Sawamura, T.; Shiraki, T.; Hosokawa, H.; Kido, T.; Hoshikawa, H.; Shimad  
 Biochem. Biophys. Res. Commun. 203, 1417-1422, 1994  
 A:Title: CDNA cloning and expression of bovine endothelin converting enzyme.  
 A:Reference number: JC2448; MUID:95032010; PMID:7945289  
 A:Accession: JC2448  
 A:Molecule type: mRNA  
 A:Residues: 1-90, 'A', 92-698, 'A', 700-758 <TM>  
 A:Cross-references: GB:S73774; NID:9688289; PIDN:AA832062.1; PID:9688290  
 C:Superfamily: neprilysin  
 C:Keywords: hydrolase; metalloproteinase; transmembrane protein; zinc  
 F:57-77/Domain: transmembrane #status predicted <TM>  
 F:595,599/Binding site: zinc, catalytic (His) #status predicted  
 F:596/Active site: Glu #status predicted

Query Match 31.5%; Score 1248.5; DB 2; Length 758;  
 Best Local Similarity 37.9%; Pred. No. 1.3e-76;  
 Matches 282; Conservative 121; Mismatches 281; Indels 61; Gaps 21;

QY 23 LVEVFGVGLVLTIFLVSQGLSLQAKQVCLKPCIEAAALISKVLSVPCDNF 82  
 DB 57 LVLVLVLAAGVLAALAGVLTQYOTRSPVCLSEACSVTSSLSMDPTVPCDF 115  
 QY 83 FFAACDGIWNNPIEDMPSYGVFWLHNDLKLKELLEKSISRRTDAIQAKILYS 142  
 DB 116 FSYACGMIKANPYDDGHSRGTFSNLMEHQALIKHLENSTA--SVSEAKRAQYYRAC 173  
 QY 143 SCMKAEKADARPLHLIHLSPFRWVLESNIGPEVWSEKRFSLQTLATRGQYSN 202  
 DB 174 ACMNTRIEELRAKPLMLIELRLG-GWNI-----TGPMDKDNFQ--DTLQVVTSHHTSP 223  
 QY 203 SFVILYSPDDKASNEHLKLDQATLSLAVREDYLDNSTAKSYRDALYFMVDTAVLLGA 262  
 DB 224 SPFEVYVSADSKNSNSNVIOVDSGLGPSRDYLL-NKTENEKVLTOGLYMMVQGLKLLG 282  
 QY 263 NS-SRAEHDKSVLRLEIKIAETIMPHENTSEAM-YNNKNISELSAMIPQDMGLYIK 320  
 DB 283 GAEDTIPRMOQILDEFETALANTITIPQEKRRDELLYHKYTAELQTLAPAIWMLPF--- 339  
 QY 321 VIOIRLPLHKDISPENNVVVRPOYFKDLFRILGSEKRTIANTLYMMRVYSRIPLN 380  
 DB 340 ---LNTIYFP--VEINSEPIVYDKETLEQISTLINTDRCLLNMYIMLVKRTSSEL 396  
 QY 381 SRRFQRMLEFSRVIOGT-TLLLPQMDKCNFIESALPYVVGKMFVDYVFOEDKEMEE 439  
 DB 397 DQRPDADAEKFMVWYGTCKTCLPRMKFCVSDTENNLGAFALGPMVKAFTFADSKSTATE 456  
 QY 440 LVEGVRAFIDMLEKENEMDAGTKRKAERAVLAKYGFPEFTM-----NDTHV 490  
 DB 457 ILLEIKKAFEEESL-STLKMDEETRKSAKERADALYNNIGYDNFTMDKEIDKYENDNTA 515  
 QY 491 DRAKIRSEADYGVNLTQTKRYLAQSDFFM-----LRKAVPTMEFTNPTVNAFYS 544  
 DB 516 DL-----YFENMRP-----FNFESWRVTADOLKRAKPNDDQSMTPPMVNAFYS 560

RESULT 8  
A:53679  
endothelin converting enzyme (EC 3.4.24.-) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text-change 20-Jun-2000  
C:Accession: A53679; J010189  
R:Shimada, K.; Takahashi, M.; Tanzawa, K.  
J. Biol. Chem. 269, 18275-18278, 1994  
A:Title: Cloning and functional expression of endothelin-converting enzyme from rat endothelium  
A:Reference number: A53679; MUID:94308045; PMID:8034569  
A:Accession: A53679  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-754 <SH1>  
A:Cross-references: GB:029683; NID:g529084; PIND:BAA06152.1; PID:g529085  
C:Superfamily: neprilysin  
C:Keywords: glycoprotein; hydrolase; metalloproteinase; transmembrane protein; zinc  
F:1-52/Domain: intracellular #status predicted <INT>  
F:53-73/Domain: transmembrane #status predicted <TM>  
F:74-754/Domain: extracellular #status predicted <EXT>  
E:129/Binding site: substrate (Arg) #status predicted  
E:150-171,194-254,300,346,367,523,616,653/Binding site: carbohydrate (Asn) (covalent) #status predicted  
E:501,595/Binding site: zinc, catalytic (His) #status predicted  
F:592/Active site: Glu #status predicted

```

Db 393 RFODADEMFEMVMTGKTKCTLPKRFKFCVSDTENNNLGFALGPMFKATPFADSKNINSEII 452
QY 440 EGVKMAFLDMLKEKENEMMDAGTKKKAKEKRAYLAKYGPFTM-----NDTHAVE 490
Db 453 LEIKAAFEESL-STLKAMWDEDTIRSAEKAADAYNNMGVYNEITMDRELDKVFENDTAYP 511
QY 491 DLKAIKFESEAVYFCGNVLOTKRYLAQSDFEFKLRAVPTEMEFTNPTLYNAFYASTQIWF 550
Db 512 DL-----YFENAKFEFNFSIKRTYADQDLKRAPNDQMSMTPPMVNAYISPTKNEIWF 562
QY 551 PAGELQKPFEMWGTEYPSRLSTGALGVIVGHEFTFGEFNNGRKYDKNGNLDPMMSTSEEEK 610
Db 563 PAGILQAPETLRSS-PAALNFGGIGVYVGHETHADDDQGREYDKONGNLPRMKKNSVYA 621
QY 611 FKERTKCALINOYSNYWKKAGLVNKGKRTLGENIADNGSLREAFRAYRKWINDROGLEE 670
Db 622 FKQOTECMVQOYNNY--SVNGEPAVNGRHHTLEINADNGSLKAYRAYQNMV--KKNGAQ 677
QY 671 PLLEGIIFTNNQLFELSYAHRCNSYRPEARQOYOLGAHSPQOFVNGAINSSEFQCA 730
Db 678 -ILFTLGLTNSQLFELFEFAQWCVSRTPRESSHGILLITDPHSRFRVIGTSLNSKSEFES 736
QY 731 FNCPPNSTYNRGMDSCRUM 749
Db 737 FRCPUGSPMN-PRKKECYW 754

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RESULT 9
S47268
endothelin-converting enzyme (EC 3.4.24.-) 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
C:Accession: S51010; S47268
R:Schmidt, M.; Kroegeer, B.; Jacob, E.; Seuberger, H.; Subkowski, T.; Otter, R.; Meyer
FEBS Lett. 356, 238-243, 1994
A:Title: Molecular characterization of human and bovine endothelin converting enzyme
A:Reference number: S51009; MUID:95104423; PMID:7805846
A:Accession: S51010
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-754 <SC2>
A:Cross-references: EMBL:Z35306; NID:9535074; PIDN:CAA84547.1; PID:9535075
C:Superfamily: neprilysin
C:Keywords: hydrolase; metalloproteinase; zinc
F:591,595/Binding site: zinc, catalytic (His) #status predicted
F:592/Active site: Glu #status predicted

Query Match          31.4%; Score 1241.5; DB 2; Length 754;
Best Local Similarity 37.9%; Pred. No. 3.7e-76;
Matches 282; Conservative 120; Mismatches 282; Indels 61; Gaps 21;

OY 23 LVVVGSGTVLGLTLLFVSGILSLQAKQKCEICKPCEIEAAALITSVNLSYDPCDNFRR 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 53 LVLVV-ALLAAALVACIAVLGIDIQYQTRTPSYSCASCIATSVSSILSSMDPTVDPGQDFET 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 83 FADCGWISNNPIPEDMPSGYGYFWLRHNVDLKLELLEKSISSRRDTEALQAKILYSSC 142
   :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 112 YACGGWIKANPVDPGDSRWGTFPSNLMEHNOALIKHLLDNSTAA--SYSEAEKQDEYYIRAC 169
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

OY 143 MNEKAIEKADAKPLIHLIRHSFFRWPLVESNIGPEGVSEKRSLSLOTLATFRGOYSNSV 202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 170 MNEIRIELKAKPLMELIERLG-GWNI-----TGPWDNDNFQ--DTLVQVTSYHTTSP 219
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 203 FIRTLYSPDDKASNEHLIKLIDQATSLAVREDYLDNSTEAKSYRDALIKFMYDPAVLIGA 262
   | :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| |||
DB 220 FFSYVYSAADSKNSNSNYIQVDQSGLGIPSKDYIL-NKTENEKVLTGYLNTMVOLGKLLGC 278
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 263 NS-SRAEDHKSVLRLEIKITAEIINIPHEKRTSEAM-YKNKNISELISAMIPQFWLGYIKR 320
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 279 GAEDTIRPQOQOILDFETALANITITPEKRRDEELIYHKYTAELQGLAIAIMWLPF--- 335
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

OY 321 VIDTRLYPHLKDIPSNSNVVYRVPQYFKDLFRILGSEKRTKTIANLYLWVRWYISRIPLWSR 380
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 336 -LNTIETP--VEINSEPIVIYDEKYLSTLINSIDKCLINMIMNLYKRTSSFLDQ 392

QY 381 RFOYMLEFSRVIOGT--TLLPOMDKCVNFIETESALPYVVGKMFVDVYFQEDKKEMEELV 439

Db 393 RQDDDEKFMEMVYTKTKTCLPRMKFCVSDIDENTLGFALGPMFVATPAEDSKNIASRTI 452

QY 440 EGVWAFIDMLEKENEMMDAGTKRRAKARAVLAKVGPFFIM-----NDTHVNE 490

Db 453 LEIKKAFEEST--STLKAMDEDTKSAKERAIDAINMIGYPNFIMDKPELDKVFNDYVAVP 511

QY 491 DLKAIKFSADYEGVNLDTKRYLAOSDFW-----LRAVAKPTMTNPTTVNAFYSAS 544

Db 512 DL-----YFNAMNR-----FNFSWRYTADOLKRAKRDQMSKTPPVNAYIYPT 556

QY 545 TNOIRPAGELQKPFMGTEYPRSLSYGAIGYVGHFTGFDNNGRKYKNDPVMWS 604

Db 557 KNEIYPAIILAPFYTRSS--PNAINFGLIGVVGHELT HARDDQGREYDKGNLRPMWK 615

QY 605 TSESEKFKTKYCMINQYSNYYWKAAGLVNKGKRTLGEMADNGSLREAFRAKRWINDR 664

Db 616 NSSVEAFKQOTACWEOXYN--SYNGEPVNGRHTLGEMADNGSLKAAVRAVQWV--K 671

QY 665 RGLLEPLPGITFTNNOLFSLYAHVRCNSYRPEAREQVOIGASHPPQFVNGAISNS 724

Db 672 KNGAEQ--TFTLGLTNNOLFSLYAHVRCNSYRPEAREQVOIGASHPPQFVNGAISNS 730

QY 725 EEFQAFNCPNPNSTNRGMDSCRW 749

Db 731 KEFSEHFHCPGSPMN--PHKCEVW 754

RESULT 10

146078

endochelin converting enzyme (EC 3.4.24.-) 2 - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 20-Sep-1999

C:Accession: 146078

R:Emoto, N.; Yanagisawa, M.

J. Biol. Chem. 270, 15262-15268, 1995

A:Title: Endochelin converting enzyme-2 is a membrane-bound, phosphoramidon-sensitive me

A:Reference number: A57042; MUID:95318093; PMID:7797512

A:Accession: 146078

A>Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-825 <EMO>

A:Cross-references: EMBL:027341; NID:g897599; PID:g897600

C:Genetics:

A:Gene: ECE-2

C:Superfamily: neprilysin

C:Keywords: hydrolase; metalloproteinase

Query Match 29.9%; Score 1184; DB 2; Length 825;

Best Local Similarity 35.1%; Pred. No. 3.4e-72;

Matches 265; Conservative 138; Mismatches 313; Indels 38; Gaps 18;

QY 4 ETGSSVETGKANKRGRTRIALVVGGLVGLTILF--LVSGQF--LSLOAKOEYCLKPECT 60

Db 102 EAGRKRTSRNLGHTQLELV--AGVSLLAALLGLGLVALGVYHNDPSHSTCTFACI 160

QY 61 EAAAILSKVNLVSDPCDNFPRACDGMISNPIPEDMPSYGYVPLRHNVDLKLELLE 120

Db 161 RVAKRIIESLDRGVSPCEDEFQFCGGMIRNPLPDGRSMNNSNSLMDNOAILKILLE 220

QY 121 KSIRRRDTEAIOKAKILYSSCMKEKAKADAKPLHLIRHSPFRPVLESNIG--PE 177

Db 221 NT--FNSSSEAKERTQRPYISCLDVERIEELGA---HALRD-----LIDKIGGNVT 268

QY 178 GVSEERKFSLLQTLATFRGOYSNVEFRLVYSPDKASNEHLIKLQDQATLSLAVREYLD 237

Db 269 GPMQODNF--MEVLKAVAGYFRAFPFLVYVSADSKSSNMIQVDSGLFLPSRDYLL-- 325

QY 238 NSTEAKSRDLKFFMVDTAVLGLANSRAHDMKSVLRLEIKTAELMIPH--EKRTSEAM 296

Db 326 NRTANKEVLAVIDYMEELGMLGGQPTSTRQOMROYLELEIOLANITVPOQDRDEKRI 385

QY 297 YNNKNISELSAMTPOPMLOIYIKKVIDTRILYPHKDISPENNVAVPOYFKLFLRILS 356

Db 386 YHKMSIAELQALAPSMOMLEFLSLSP-----LELGSEPVVYGTDLQGVSELINR 439

QY 357 ERKRTINLVYWRVYSRINLSRRFOYRWLEFSRVIOGT--TLLPOMDKCVNFIETESALP 415

Db 440 TEPVNLNLYLWNLVQTTSSLDHREFSADKLETLTYGKKKCTPRMOCISINTDQALG 499

QY 416 YVVGKMFVDVYFQEDKKEMEEIVEGVWAFIDMLEKENEMMDAGTKRRAKARAVLAK 475

Db 500 FALGSLFPAKTFDQSKSEIAGMISEIRVAFEAL--GHLVWMDKTEFOAKERAADAIYDM 558

QY 476 VGYPEFTIMNDTHVEDLKAIFSEADYFGVNLDTKRYLAOSDFWTLKAVPKTEWFTNPT 535

Db 559 IGFPDFLEPKELDDYDGYEVSEDSFQNNLNYNSAKVMADOLKPPSRQMSKTPQ 618

QY 536 TVNAFYSASTQIRPAGELQKPFMGTEYPRSLSYGAIGYVGHFTGFDNNGRKYDK 595

Db 619 TVNAYILPTKNEIYFPAGILAPFY--TGNHPQALNFGIGVVGHELT HARDDQGREYDK 677

QY 596 NGNIDPMWSTSESEKFKTKYCMINQYSNYYWKAAGLVNKGKRTLGEMADNGSLREAFR 655

Db 678 EGNLRPMWQNSLAFRNRHTACIEOYSQY--QVNGEKRLQRTLGEMADNGSLKAAV 735

QY 656 AYRKWINDROGLEEPLPGITFTNNOLFSLYAHVRCNSYRPEAREQVOIGASHPPQF 715

Db 736 AYKAWL--RKHG--EQQLPAGVGLNHLQFLFYGFAVWMSVTPRESSHGLTDPHSAPF 792

QY 716 RVNGAISNSEEFQAFNCPNPNSTNRGMDSCRW 749

Db 793 RVLGTLNSRDFLRHFGCPVSGPMNSG--QLCEVW 825

RESULT 11

DB8082

protein T05A8.4 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001

C:Accession: DB8082

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio

A:Reference number: A75000; MUID:99069613; PMID:9851916

A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C-

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;

A:Accession: DB8082

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-750 <STO>

A:Cross-references: GB:chr\_II; PIDN:AB95021.1; PID:g2746865; GSPDB:GN00020; CESP:T05A

C:Genetics:

A:Gene: T05A8.4

A:Map position: 2

C:Superfamily: neprilysin

Query Match 28.3%; Score 1119.5; DB 2; Length 750;

Best Local Similarity 32.4%; Pred. No. 7e-66;

Matches 250; Conservative 150; Mismatches 324; Indels 47; Gaps 15;

QY 2 EAETGSSVETGKANKRGRTRIALVVGGLVGLTILF--LVSGQF--LSLOAKOEYCLKPECT 57

Db 4 DEEDGTTKSPG--SHWIRIMAILILILFLVGAIVYR---YINWKSSDVCISP 56

QY 58 ECTEAAAILSKVNLVSDPCDNFPRACDGMISNPIPEDMPSYGYVPLRHNVDLKLE 117

Db 57 GCIKTAVLSLSSNSVYDCDDPFYERACGOWIKGHIIPDARASVNSFENLGGDLFAKLE 116

QY 118 LT--EKISIRRRDTEAIOKAKILYSSCMKEKAKADAKPLHLIRHSPFRPVLESNIGP 176

Db 117 LTDENDPEPYDETSAVGAKAYFYNLCLINSEIILDNRTTFDEYVK--SFGGWPSLSGHOMKP 175



Oy 177 EGWSEKRSLSQTLATTFPGQGVSNVFLRLVYSDDDKASNEHIKLDQATLSIANREDYL 236  
 Db 176 DA-----SIEMLYADWAKKADSLFKAVQDPDKRSRHHLLIDQDPLMFADFVY 228  
 Oy 237 DNSTEAKSYRDALYKEMVDYAVLIGANSSRAEHMKSVLLEKIAEIMPHENRSEA- 295  
 Db 229 AAEENE---RMAYLQILIRVILLDLADDRATLDAKEIIDFETALNITMADEHRIADAE 285  
 Oy 296 MYKMNISELSAMIPQFMGLGIRKIVDTRLPLKIISEN--VYRVPOYQKDLERI 353  
 Db 286 LYRKITLIGEKRSLSPEHMPLEPNMEKDLHEKKKITIDDTDETVYVYGYEFLRLDYL 345  
 Oy 354 LGSERKTIANYLVWRMYV-SNIPULSRFOYRMLEFSRYIQGTTLPLQPMCKVNFIES 412  
 Db 346 IPQYDNRLLIVNLECMQEFFKTMRLDLPDPALFTLFKKYKTLNIMNQYRMHGCTRLNS 405  
 Oy 413 ALDYVYVKFVYVYVYQEDCKEMMEIEVGRMAFIDMLEKEMNDMADGCKRAKAKARAV 472  
 Db 406 LHMWATSAIYVANHDEHAKQVDEMSLIMESVFDLLSE-DMLTKETQAKOKRVEM 464  
 Oy 473 LAKVGPPEIIMDTHVNEEDLAKIFESADYFGVNLQTRKYLQSDPFMRKAVPKTEMT 532  
 Db 465 KRKIGPYDLNPAVYVNYETFFVYVGHYVYQKFSFYEDQYRDVLEKTEAVDEREYVA 524  
 Oy 533 NPTVVAEFSASTNQIR-----FAGELQKPFPMGTEYPRSLSYGAIGYIV 578  
 Db 525 GAELVNAEFSPTNTEISKFLGTLTQKKEFSVFAGILQ--PVFYSKDFPSNMFGIGYVI 583  
 Oy 579 GEHFTGCPDNQNRKDKKNGINDPWPMSSESEKREKTKCMINQSYNYWKAKAGLVNGKR 638  
 Db 584 GHEITHGPDGRLYDLNNGIRQWMDNATISKREHKAQCLEKQSYVLDQINMQIGKS 643  
 Oy 639 TIGEMIANDNGCIREAFYRKWRINDRQGLEEPLRLPGITFTNNOLFSTVAHRCNSYRP 698  
 Db 644 TIGEMIANDNGCIGLKAAYRKYK---EKRRHSPRPRLPGVMLTDHOLFETVAIQMGCTWD 700  
 Oy 699 EBARQVQVIGAHSPPOFVNGAISNSEEPKAPCNPNSTNMRGSDSRLW 749  
 Db 701 KRAIKRLTSHSPGPIRVKGPGLSNSIDPKAKVNCPEGSQMN-PREKCRW 750

RESULT 12  
 T20003  
 hypothetical protein ZK20.6 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_rev1sion 15-Oct-1999 #text\_change 21-Jan-2000  
 C:Accession: T20003; T27775  
 R:Gajadasy, S.  
 submitted to the EMBL Data Library, March 1996  
 A:Reference number: Z19209  
 A:Accession: T20003  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-766 <WIL>  
 A:Cross-references: EMBL:Z69902; PIDN:CAA93770.1; GSPDB:GN00020; CESP:ZK20.6  
 A:Experimental source: clone C4/D12  
 R:Gajadasy, S.  
 submitted to the EMBL Data Library, March 1996  
 A:Reference number: Z20417  
 A:Accession: T27775  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-766 <NI2>  
 A:Cross-references: EMBL:Z69904; PIDN:CAA93782.1; GSPDB:GN00020; CESP:ZK20.6  
 A:Experimental source: clone ZK20  
 C:Genetics:  
 A:Gene: CESP:ZK20.6  
 A:Map position: 2  
 A:Intons: 11/1; 334/3; 439/1; 692/2; 734/2  
 C:Superfamily: neprilysin

Query Match	25.68;	Score 1014.5;	DB 2;	Length 766,
Best Local Similarity	31.88;	Pred. No. 9.6e-61;		

	Matches	223;	Conservative	157;	Mismatches	292;	Indels	29;	Gaps	17;
QY	61	EAAAIILSKVLSDPCDNFFRFACDGMISNNPIPEDMSTGYVPLWLRHNYDLKLKELLE	120							
Db	83	EASLLQKSLNLSDPCDDDFEYACRAWVSHPIPDLLTYSQPTAAKREKVLAEHRKLYE	142							
QY	121	KSISRARDTEAIOAKILLYSCSMEKEAIKRDAPCLHLIRHSPFRMPVLSENIGPCSGW	180							
Db	143	DNWS-IPTKSIALIKOILYTMCDTEKHNNAVGAADLLKIKITYY-WPWNHNE-----KW	195							
QY	181	SERFSLQLLAFPRGOYSNVFIRLYVSPDDKASNEHILKLDQATLSL--AVREDYLDN	238							
Db	196	RESFEDTLKLSTIGSDRVSVFEFGPADSRVNSRRLLSFQSGIGLGYSTRDYLYDE	255							
QY	239	---STEAKSYRD--ALYKFMVDATVLLGANSNSAEHDMKVLTREKIAEIMPHENRT	292							
Db	256	KYKYEKQKAVRKTYIGKVRYYTEDAG-MAYNNEKIESDVEDIILAEKEMOILVAEEDRR	314							
QY	293	S-EAMVYKMMISELSAMIPQDWLGVIKKVYIDRLYPLHLDISPSENVVVRVQYERDLF	351							
Db	315	NYTKLVNRRFDDLKEYMSIIDWKLLSTTPFLVHSYLK-TWPS--IISDVEYLQKM	371							
QY	352	RIGSEKKTIANYLIVRWVYSRILPNLSRFQYRMLEFSVIGTITLLPQMKCVNETE	411							
Db	372	TLLQNDPRLVTYIIILNAGMSQSGELGKYIEDLQDFAFQMGRKOROPRMDCVSSAG	431							
QY	412	SALPIYVVGKMFVDVYFOEDKKEEMEEVLVEGVRAFTDMLTEKENEMDAGTKRKKAKARA	471							
Db	432	GKLSYASGSYVYKRYEDANAKNITLLDITDLOAFRNMH--ANDWMDAETKKALELKAQ	490							
QY	472	VLAQVYEPFIMMDVHVEDLKAIKFSEADYFENNVLOTKRYLAQSPFWLR--KAVPKIE	529							
Db	491	MUKOIGYPRPILNDEKLDMDYKGLGAPEDSISQVLE-KSIQWRNNFYRRLLEPVRNRE	549							
QY	530	WFTNPITVNAFYSASTNOIRFPAGELQKPEFMWETEPRSLSYGAIVIGHEFHGFDNN	589							
Db	550	FISLSAAVNAFASPTNNALAFRAGILQPPF--DARPPKALNGGICAVIGHETHFDPT	608							
QY	590	GRRYDANGMLDPMWSTESSEKFEKTKKMIINOYSNTYMKKAGLVNKGKTLGENTADNG	649							
Db	609	GROFDWAGLBRWDNTTJSKFERKQOCILIEQYADVKKGLDRLRNGKLTQGBENTADNG	668							
QY	650	LEAEFAYRKWLNDRRQGLEEPLDPI-TFTNNQLEFSLYAHVRCNSYPEAAREQVQIG	708							
Db	669	IKOAFKAYKSYL--EKHGQGEARLPQESLJTEQOLFVEVQAQVWGCAKPEPKITLLILD	726							
QY	709	AHSPQFVRNGAISNSEEFQAFNCPBNPNTSMRGMDSCILM	749							
Db	727	PHSPETAKVNYVLINQPEAEAFKCPAGSPM--PTKKCVVM	766							

```

RESULT 13
C880099
protein F18A12.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence-revision 10-May-2001 #text-change 10-May-2001
C:Accession: C880099
R:anonymous: The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bid
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.mutl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C
A:Accession: C880099
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <STO>
A:Cross-references: GB:chr_II; PIDN:AB66079.1; PID:g2315629; GSPDB:GN00020; CESP:F18A
C:Genetic:
A:Gene: F18A12.8
A:Map position: 2

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Query Match	25.28; Score 997; DB 2; Length 590;
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QY 54 CLKPCIEAAAAILSKVNLSDPCDNFFRFACDGMISNNPIPEDMPSGYVY PMLRHN-- 111

[illegible]

:	:	:	:	:
:	:	:	:	:
:	:	:	:	:

00 163 HSPBBDVT ESNICBEGVWS ---FBKESLJOTV ATEPCOVNSVETBI VVSPDDKASNEH 318

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Db      193  RIG-GWPTLEGDKWOF--WSHSWEEOIALVNLTV-----NAVILEMAVTHDPSNSSRS 244
          ||| : | : : : ||| : : : ||| :

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QY 219 ILKIDQATLSLAVREDYLD--NSTEAKSYRDALYKFMVDTAVLLGANSRAEHDMKSVLR 276

Db 245 VIELDQPKWGAGSRYPYLSGANDPMLRNYT---TLMKMTAVALGADPAIAEKEMNEAME 3000

277 LEIKI-----AEIMPHENRTSEAMYNKNISLSAMIPQFDWLG YIKKVIDTRLYPHLKD 332

Db 301 FELKLVNESADDMV---RRDPERGNNRFEELWQLKSVFPEINEEKYKTV-----FKELVA 352

333 ISPSENVWRPQYFKDLFRILGSEKRTIANYLWRRMYSRIPNLSRRFQYRWLEESRV 392

00 303 25FNH1V1VKEIDIEFGIYGHVZQSIFFNNVLRANI15MNLVWQGF3FFFFFSKNEFFI1QFNKN 412

[illegible]

1

473 1U-VI DEDVCEITBPBPA TSKANMTEVKSCEBMUT ENDTIMERN- WCMITKD 520

QX 510 RXYIAO-----SDEFWI RKAVPKTEWETNPPTVNAFYSASTNOTRBPAGFI OKP 558

Db 521 REYLLHTIRVKLVRFTEELLRLDOPIDRSMWFOSPAVDAYAPNNNEMIFPAGIMOF 580

559 FFWGTEYPRSLSYGAIGVIVGHEFTHGFDNNGRKYDKNGNLDPWSTESESEKFKETIKCM 618

Db 581 FL-TLGVPNYITYGMVGAVIGHEVSHAFDDGGQYDENGNLNDWDAETEKEFIEKTRCF 639

619 INQSYNYWKAGLNKGRITLGENIADNGGLREAFRAYRKWINDRQGLEEPLPGI-T 6777

Db 640 VROEYVHVVEADIHNLGQLSGENIADNGGVKTA FNAYKAW-KSNTTGISEPALPGFQN 698

0/8 FINNQFFLSIAHVKNISIRPEAREQVQIGAHSPQFRVNGAISNSEEFQKAFNCPPNS /3/

[illegible]

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	..	..	
	—	—	

RESULT 15  
F87683

C:Species: Caulobacter crescentus  
peptidase M13 family protein [Imported] - Caulobacter crescentus

C;Accession: F87683

B. ; Laub, M.T. ; DeBoy, R.T. ; Dodson, R.J. ; Durkin, A.S. ; Gwinn, M.L. ; Haf-

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Reference number: A87249; MUID:21173698; PMID:11259647  
A;Accession: E87683

A;Status: preliminary  
A:Molecule type: DNA

A; Residues: 1-706 <SIO>  
A; Cross-references: GB:AE005673; NID:q13425232; PIDN:AAK25466.1; GSPDB:GN0

A;Gene: CC3504

Page 9

Query Match	20.6%;	Score 814.5;	DB 2;	Length 706;
Best Local Similarity	30.6%;	Pred. No. 3.1e-47;		
Matches 229;	Conservative 109;	Mismatches 316;	Indels 95;	Gaps 20;

QY	40	VSOGSLSLQAOEY-CLKEPECI-----BAAAI-----LSKNLS	73
Db	14	LSLSAFGQAHEKHAACIDDACVMSQLPSTTAGAAMDVASLESREPCWGFDSGMDTY	73
QY	74	VDPCDNFEFACDGMWISNNPIPEDMPSYGYVWLRHNVDLKLKELLEKSISRDRDEAIQ	133
Db	74	VKPEDGEFFKANGAMDARTQJPSDRTRXGNDKLAELSEARTKAIIPAAANAKATGDTA	133
QY	134	KAKIITYSSCMNEKAIERADAPLHLIRHSFRRPVULESNIIGPBGVSEKRFSLQTLAT	193
Db	134	KVGAAYRFEMDEAGIEKIDAPFI-----APYIAEI-----RKVRSKDEFTT	174
QY	194	FRGQSVNSF---IRLYSPDDKASNEHILKLDQATLSLAREDYLDNSTEAKSYRATY	250
Db	175	LMGSSSTTFPSLSGLGSTDAKKPKAYVYAGAGGSLSDPRODYLDAKRADKK---AAY	231
QY	251	KFWYDVAVLGANSRAEHDKSVLRLEIKIAETIMPH-ENRTSEAMYNKMNISELSAMT	309
Db	232	LAYEKLTLTMAGMDKPAEH-AKAVYDEETKLAETWYTRAEERDRDKTYNPATIALEQAMS	290
QY	310	POFOMLGIVKIVDTRLYLPHLKDISPBNVYVRVQYFKDLEFRLTGERKKITANIYIMR	369
Db	291	PGYOWNRITA-----ASGLPKVDFRVVTTNTTFPRYAKIYAEPLDITLKAQAFK	340
QY	370	MYGSRIPILSRFQYRWLEF-SRVIOGTTTLTPQMDKCVNFIESALVYVGNKFEVDVYFQ	428
Db	341	VTDNAPRLTSKRFVDAGEFENKTKLQAQPEDRPMKRGYGVANGVLGEANGKDYAAIYF	400
QY	429	EDKKEMMEELVEGYRWAF--IDMLERENEMWAGTRKRAKERAVALARVGYPEFTIMD	485
Db	401	PESKAKMELIYANVRGAAMKVRIDNL-----DMSAETRYVKAQEKLAKFTVYIGPD	451
QY	486	THVWEDLKATFSEADYFNGVNLQTRKTLAQSDFFWLLKAPKTEBMFTNPPTVNAAFYSAST	545
Db	452	--VVEDSKLEIKINDYAGNVQRGAWAFAKADVERLKPVDKTEMGWTPDTVAAYNSVN	509
QY	546	NOIRFPAGELQKPEFWMGTEYPRASLYGALIGVYHEFTHEDDNNGRKYDNGINDPMWST	605
Db	510	NEIYFPAALLOAPFFHPDAP-AINTYGGIGVISHETHEGFDQGRKSDGCVLRDWMITA	568
QY	606	ESEEFKEKTEKCMITNOYSNYYWKKAGLVNKGKRTLGENIADNGSLREAFRAYRWINDRR	665
Db	569	EDAAKFKQAODRLCAQGAFE-PLPGKKLNGALTMGENIDMGGLARFALDAYRASL----	623
QY	666	QGLEEPLIPGTTTFNNQFLSTYAHVKNSTRPRAAREQVOIGAHSPQEFRRVNGAISNSE	725
Db	624	KGQAPAPYLDG--FPGDQRYVLGMQVWRGQORDEALKOQIILAGPHSGYRVANGTIRNME	681
QY	726	EFOKAFNCPNSTM-----NRGMDSCRLT	749
Db	682	GWYSATIDKPEDKLIYAPENK-----VATM	706

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Job time : 52 secs